GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 2, 2005, 14:31:47 ; Search time 341.745 Seconds
(without alignments)
7937.378 Million cell updates/sec

Title: US-09-979-558A-1
Perfect score: 1526
Sequence: 1 tttgatcatggctccagatt.....acctgcggctggatcacctc 1526

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	1211	79.4	269223	3	US-09-596-002-41	Sequence 41, Appl
	2	1195	78.3	1485	2	US-08-299-810A-27	Sequence 27, Appl
	3	1098.6	72.0	1501	3	US-09-793-920A-1	Sequence 1, Appli
	4	1098.6	72.0	1501	3	US-09-821-016-5	Sequence 5, Appli
	5	1098.6	72.0	1501	3	US-09-745-476-1	Sequence 1, Appli
	6	1098.6	72.0	1501	3	US-09-748-205-1	Sequence 1, Appli
	7	1098.6	72.0	1501	3	US-09-951-720-1	Sequence 1, Appli
	8	1098.6	72.0	1501	3	US-10-411-319-1	Sequence 1, Appli
	9	1098.6	72.0	1501	3	US-10-105-305-1	Sequence 1, Appli
	10	1098.6	72.0	1501	3	US-10-266-787-5	Sequence 5, Appli
	11	1098.6	72.0	1501	3	US-09-791-610-1	Sequence 1, Appli
	12	1098.6	72.0	1501	3	US-10-252-518-5	Sequence 5, Appli
	13	1076	70.5	1542	2	US-08-114-695A-1	Sequence 1, Appli
	14	1073.8	70.4	1481	3	US-09-737-297-4	Sequence 4, Appli
	15	1070.8	70.2	1467	3	US-09-726-774-3	Sequence 3, Appli
	16	1069.2	70.1	1542	2	US-08-757-653-158	Sequence 158, App
	17	1069.2	70.1	1542	3	US-09-465-355-2	Sequence 2, Appli
	18	1069.2	70.1	1542	3	US-08-520-946-158	Sequence 158, App
	19	1069.2	70.1	1542	3	US-09-655-378A-158	Sequence 158, App
	20	1069.2	70.1	1542	3	US-09-548-998E-33	Sequence 33, Appl
	21	1069.2	70.1	1542	3	US-10-061-071-33	Sequence 33, Appl
	22	1062.6	69.6	1541	3	US-09-726-774-2	Sequence 2, Appli
	23	1058.2	69.3	1549	3	US-09-492-709A-89	Sequence 89, Appl
	24	1058.2	69.3	1549	3	US-09-492-709A-242	Sequence 242, App
	25	1058.2	69.3	1549	3	US-09-492-709A-402	Sequence 402, App
	26	1053.6	69.0	1518	2	US-08-114-695A-6	Sequence 6, Appli
	27	1052.4	69.0	1487	3	US-09-726-774-14	Sequence 14, Appl
	28	1046.8	68.6	1424	3	US-10-007-527A-12	Sequence 12, Appl
	29	1039.2	68.1	1506	3	US-10-278-942-1	Sequence 1, Appli
	30	1039.2	68.1	1506	3	US-10-694-352-1	Sequence 1, Appli
	31	1031.2	67.6	1500	3	US-09-726-774-4	Sequence 4, Appli
	32	1027.8	67.4	1486	3	US-09-737-297-1	Sequence 1, Appli
	33	1025.2	67.2	1544	3	US-09-726-774-5	Sequence 5, Appli
	34	1019.8	66.8	1540	3	US-09-228-184-1	Sequence 1, Appli
	35	1019.8	66.8	1540	3	US-09-967-376-1	Sequence 1, Appli
	36	1016.4	66.6	1429	3	US-09-934-868-81	Sequence 81, Appl
	37	1016.4	66.6	1429	3	US-10-701-200-81	Sequence 81, Appl
	38	1014.8	66.5	640681	3	US-09-790-988-1	Sequence 1, Appli
	39	1008.8	66.1	1830121	3	US-09-557-884-1	Sequence 1, Appli
c	40	1008.8	66.1	1830121	3	US-09-557-884-1	Sequence 1, Appli
	41	1008.8	66.1	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c	42	1008.8	66.1	1830121	3	US-09-643-990A-1	Sequence 1, Appli
	43	1008.8	66.1	1830121	3	US-10-158-865-1	Sequence 1, Appli
c	44	1008.8	66.1	1830121	3	US-10-158-865-1	Sequence 1, Appli
	45	1004.2	65.8	1484	2	US-08-632-470-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-596-002-41/c
; Sequence 41, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 269223
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte template ID No. 6632636 41
; PUBLICATION INFORMATION:
US-09-596-002-41

Query Match 79.4%; Score 1211; DB 3; Length 269223;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 127; Indels 15; Gaps 6;

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Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
                  | ||||||||||||||||  ||||||||||  ||||||||||||||||||  ||  |||
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Db      92840 GAAACCCAAGCTAATACCGCATACGACCTACGGGTGAAAGGGGG----CTTTTAGCTCTC 92785

Qy        210 GCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCGA 269
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Db      92784 GCTATTAGATGAGCCTAAGTCGGATTAGCTGGTTGGTGGGGTAAAGGCCTACCAAGGCGA 92725

Qy        270 CGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGAC 329
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Db      92664 TCCTACGGGAGGCAGCAGTGGGGAATATTGGATTGGACAATGGGCGAAAGCCTGATCCAG 92605

Qy        384 CCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGA 443

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Qy        564 GCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGC 623

Db      92424 GCGCGCGTAGGTGGTTATTTAAGTCAGATGTGAAAGCCCCGGGCTTAACCTGGGAACTGC 92365

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Qy        864 TAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGC 923

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Db      92004 CATAGTGAGAATCTTGCAGAGATGCGAGAGTGCCTTCGGGAATTCACATACAGGTGCTGC 91945

Qy       1044 ATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC 1103

Db      91944 ATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC 91885

Qy       1104 TTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTG 1163

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Qy       1164 GAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGC 1223

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Qy       1464 GTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

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Qy       1524 CTC 1526

Db      91465 CTC 91463
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RESULT 2
US-08-299-810A-27
; Sequence 27, Application US/08299810A
; Patent No. 5721097
;  GENERAL INFORMATION:
;    APPLICANT:  Rossau, Rudi
;    APPLICANT:  Van Heuverswyn, Hugo
;    TITLE OF INVENTION:  HYBRIDIZATION PROBES FOR THE
;    TITLE OF INVENTION:  DETECTION OF BRANHAMELLA CATARRHALIS STRAINS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 No. 5721097west Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/299,810A
;      FILING DATE:  01-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hillson, Randall A.
;      REGISTRATION NUMBER:  31,838
;      REFERENCE/DOCKET NUMBER:  8076.70-US-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1485 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Branhamella catarrhalis
;    IMMEDIATE SOURCE:
;      CLONE:  16S rRNA Gene
US-08-299-810A-27

  Query Match             78.3%;  Score 1195;  DB 2;  Length 1485;
  Best Local Similarity   90.6%;  Pred. No. 0;
  Matches 1352;  Conservative    0;  Mismatches  128;  Indels   12;  Gaps    7;

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Qy         96 CCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGGGAAACT 155

Db         57 GCGGACGGGTGAGTAATGCTTAGGAATCTGCCTAGTAGTGGGGGATAACTTGGGGAAACC 116
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Qy       216 AGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCGACGATCT 275
Db       173 AGATGAGCCTAAGTCGGATTAGCTGGTTGGTGGGGTAAAGGCCTACCAAGGCGACGATCT 232

Qy       276 GTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGACT-CTAC 334
Db       233 GTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTAC 292

Qy       335 GGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCATGCCGCGT 394
Db       293 GGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGT 352

Qy       395 GTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCTTCGGTTA 454
Db       353 GTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGTGGGGAGGAAAAGCTTATGGTTA 412

Qy       455 ATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGCCAGCAGC 514
Db       413 ATACCCATAAGCCCTGACGTTACCCACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGC 472

Qy       515 CGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGTAGG 574
Db       473 CGCGGTAATACAGAGGGTGCAAGCGTTAATCGG-ATTACTGGGCGTAAAGCGCGCGTAGG 531

Qy       575 TGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCTGAAACTG 634
Db       532 TGGTTATTTAAGTCAGATGTGAAAGCCCCGGGCTTAACCTGGGAACTGCATCTGATACTG 591

Qy       635 TTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATGCGTAGAG 694
Db       592 GATAACTAGAGTAGGTGAGAGGGGNGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAG 651

Qy       695 ATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTGAGGCTCG 754
Db       652 ATCTGGAGGAATACCGATGGCGAAGGCAGCTCCCTGGCATCATACTGACACTGAGGTGCG 711

Qy       755 AAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCTA 814
Db       712 AAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCTA 771

Qy       815 CTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGACCGCCTG 874
Db       772 CCAGTCGTTGGGTCTTTTAAAGACTTAGTGACGCAGTTAACGCAATAAGTAGACCGCCTG 831

Qy       875 GGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGG 934
Db       832 GGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGG 891

Qy       935 AGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATACACAGAA 994
Db       892 AGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATAGTGAGAA 951

Qy       995 TCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGGCTGTCGT 1054
Db       952 TCTTGCAGAGATGCGAGAGTGCCTTCGGGAATTCACATACAGGTGCTGCATGGCTGTCGT 1011

Qy      1055 CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTTAGT 1114
Db      1012 CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTTTCCTTAGT 1071

Qy      1115 TACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAGGAAGGCGG 1174
Db      1072 TACCAGCGACTCGGTCGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAGGAAGGCGG 1131

Qy      1175 GGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGTAG 1234
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Qy      1235 GTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCGTAGTCCAG 1294

Db      1192 GTACAAAGGGTTGCTACACAGCGATGTGATGCTAATCTCAAAAAGCCAATCGTAGTCCGG 1251

Qy      1295 ATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGATCAGAATG 1354
Db      1252 ATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGCAGATCAGAATG 1311

Qy      1355 CCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGATT 1414
Db      1312 CTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTGATC 1371

Qy      1415 GCACCAGAAGTGGTTAGCCTAACTTAGTGAGGGCGATCACCACGGTGTGGTCGATGACTG 1474
Db      1372 TCACCAGAAGTGGTTAGCCTAACGCA-AGAGGGCGATCACCACGGTGGGGTCGATGACTG 1430

Qy      1475 GGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCTC 1526
Db      1431 GGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAA-CTGCGGCTGGATCACCTC 1481
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RESULT 3
US-09-793-920A-1
; Sequence 1, Application US/09793920A
; Patent No. 6479621
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as
; TITLE OF INVENTION: monomer unit, and method for producing the same.
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/793,920A
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-793-920A-1

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Qy        30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db         9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy        90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db        67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy       150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
Db       124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy       209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
Db       184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy       269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
Db       244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy       329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
Db       304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy       388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
Db       364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy       448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
Db       424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483
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Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
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Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||| |||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
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Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
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Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              |||||  |||||  |||||||  |||||||  |||||||||||||  |||||  ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              ||||||||||||||||||||||  ||||||||||||||||||||  ||  ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||   ||| ||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              |||||||||||||||  |    |||||| ||||||||| |||||| |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              |||||  ||||| ||||||||||||||||||||||||||||| || ||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              ||||||  ||||||||||   ||  |  | |||| |||  ||  |||| ||  ||| ||  ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              ||||||  |||  | ||||||||||||||  |  ||||||  |||||||||||||||||  |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              |||  |  ||||||||||||||  |  |||  |||| |||  |  ||||  ||  |  ||||||||||  |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
                ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 4
US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. 6485951
; GENERAL INFORMATION:
;  APPLICANT: CANON INC.
;  TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
;  FILE REFERENCE: 4051021
;  CURRENT APPLICATION NUMBER: US/09/821,016
;  CURRENT FILING DATE:  2001-03-30
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Microsoft Word
; SEQ ID NO 5
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii P161 ; BP-7376
;   FEATURE:
US-09-821-016-5

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| ||||||||||||||||||||  | || |  |||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | ||||||||||||||||| | |||||||| ||| ||||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              ||||||  |||||||||||  |||||||||||||  |||||  |||||  |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              ||||||  |||  ||||||||||||||||||||||||  |||||  || ||||||||||||  || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              ||  |||||||||||||||||||||||||||||||||||  | ||  ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||  |||  | ||||||||||||||||  | ||  ||||  |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |    ||||  |||  |  ||||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||| |||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||||  |||||||  |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              ||||||  ||  |||||||  |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
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Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 5
US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. 6521429
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hidroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143
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Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 6
US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. 6586562
; GENERAL INFORMATION:
;  APPLICANT:  Canon Inc.
;  TITLE OF INVENTION:  Polyhydroxyalkanoate its manufacturing method, and microorganism
;  TITLE OF INVENTION:  those are used for the method.
;  FILE REFERENCE:  4351009
;  CURRENT APPLICATION NUMBER: US/09/748,205
;  CURRENT FILING DATE:  2000-12-27
;  NUMBER OF SEQ ID NOS:  1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAAACCCTGATCCAGCCAT 387
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 7
US-09-951-720-1
; Sequence 1, Application US/09951720
; Patent No. 6635782
; GENERAL INFORMATION:
;  APPLICANT: Canon Kabushiki Kaisha
;  TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof
;  FILE REFERENCE: 4477001
;  CURRENT APPLICATION NUMBER: US/09/951,720
;  CURRENT FILING DATE:  2000-09-14
;  PRIOR APPLICATION NUMBER: JP 279900/2000
;    JP 378827/2000
;    JP 165238/2001
;    JP 165509/2001
;    JP 275063/2001
;  PRIOR FILING DATE: 2000-09-14
;    2000-12-13
;    2001-05-31
;    2001-05-31
;    2001-09-11
;  NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii P161 strain.
US-09-951-720-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| ||||||||||||||||||||  | || |  |||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | |||||||||||||||| | |||||||||| ||| ||||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||||| ||||| ||||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||||||||||| ||||| || ||||||||||| || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || |||||||||||||||||||||||||||||||||||||  | || ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||  | ||||||||||||||||  | || ||||     |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||     |      |||| ||| |  ||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  ||||||||| ||||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||||| |  ||||||  || |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              ||||||  ||  |||||||  |||  |||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              |||||  |||||  |||||||   |||||||  |||||||  |||||||||||||  ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||| |||||||||||||||||||  || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||||   ||| ||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
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Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
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Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
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Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              ||||||  ||||||||||||  || |  | |||| |||  ||  |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              ||||||  ||| | |||||||||||||||| | ||||||  ||||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
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Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 8
US-10-411-319-1
; Sequence 1, Application US/10411319
; Patent No. 6649381
; GENERAL INFORMATION:
;  APPLICANT: Canon Inc.
;  TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganism
;  TITLE OF INVENTION:  In The Same
;  FILE REFERENCE: 03500.015001.1
;  CURRENT APPLICATION NUMBER: US/10/411,319
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: US 09/748,205
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;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||||  | || |  |||||||| |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | ||||||||||||||| | ||||||||| ||| |||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||||| ||||| ||||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||| ||||| || |||||||||| || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || |||||||||||||||||||||||||||||||||  | || ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||   | |||||||||||||||  | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |      |||| ||| |  ||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||||| |||||||||  ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
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Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
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Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
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Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
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Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
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Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||||||||| |||||||||||||||||| || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||   ||| ||||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              ||||||||||||||||  |    |||||| |||||||||| ||||||  |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| ||||| |||||||||||||||||||||||||||| || ||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
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Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
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Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
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Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
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Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 9
US-10-105-305-1
; Sequence 1, Application US/10105305
; Patent No. 6777153
; GENERAL INFORMATION:
;  APPLICANT: CANON KABUSHIKI KAISHA
;  TITLE OF INVENTION: POLYHYDROXYALKANOATE CONTAINING UNIT WITH THIENYL STRUCTURE IN TH
;  TITLE OF INVENTION:  CHAIN, PROCESS FOR ITS PRODUCTION, CHARGE CONTROL AGENT, TONER B
;  TITLE OF INVENTION:  TONER WHICH CONTAIN THIS POLYHYDROXYALKANOATE, AND IMAGE-FORMING
;  TITLE OF INVENTION:  IMAGE-FORMING APPARATUS WHICH MAKE USE OF THE TONER
;  FILE REFERENCE: CFO16309
;  CURRENT APPLICATION NUMBER: US/10/105,305
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: JP 2001-090026, JP 2001-133551
;  PRIOR FILING DATE: 2001-3-27, 2001-4-27
;  NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain.
US-10-105-305-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||||  | || |  |||||||| |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
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Db        67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

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Db       124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy       209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db       184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy       269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db       244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy       329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGNGGGAACCCTGATCCAGCCAT 387

Db       304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy       388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db       364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy       448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db       424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy       508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db       484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy       568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db       544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy       628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db       604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy       688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db       664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy       748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db       724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy       808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db       784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy       868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db       844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy       928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db       904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy       988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db       964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy      1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db      1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy      1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db      1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy      1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db      1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy      1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db      1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy      1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db      1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy      1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db      1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy      1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db      1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy      1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db      1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 10
US-10-266-787-5
; Sequence 5, Application US/10266787
; Patent No. 6808910
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Honma, Tsutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 03500.015225.3
; CURRENT APPLICATION NUMBER: US/10/266,787
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: JP 2000-095004
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
; FEATURE:
; FEATURE: cDNA to 16S rRNA
US-10-266-787-5

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Qy        30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db         9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy        90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db        67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy       150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db       124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy       209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db       184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy       269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db       244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy       329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
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Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              ||||||||||||||||||| |||   | |||||||||||||||||   | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |      |||| ||| |  ||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  ||||||||| ||||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||||  |||||  || |||||||  ||||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              ||||||  ||  |||||||  |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              ||||| ||||| |||||||  |||||||  ||||||| ||||||||||| ||||| ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||| |||||||||||||||||| || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||     | ||||||||||||    ||| ||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              |||||||||||||||  |   |||||| |||||||| |||||| |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| ||||| ||||||||||||||||||||||||||| || ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              |||||| ||||||||||   || |  | |||| |||  || |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              |||||| ||| | |||||||||||||||| | |||||| |||||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | |||||||||||||| | ||| |||| ||| | |||| || | ||||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 11
US-09-791-610-1
; Sequence 1, Application US/09791610
; Patent No. 6861550
; GENERAL INFORMATION:
;  APPLICANT: Canon Inc.
;  TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid as
;  TITLE OF INVENTION:  monomer unit, and method for producing the same.
;  FILE REFERENCE: 4396021
;  CURRENT APPLICATION NUMBER: US/09/791,610
;  CURRENT FILING DATE:  2002-09-30
;  NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-610-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 0;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| ||||||||||||||||||||  | || |  ||||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | |||||||||||||||| | ||||||||| ||| ||||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||||| ||||| ||||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||| ||||| || |||||||||||  || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || |||||||||||||||||||||||||||||||||||||||  | || ||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||   | |||||||||||||||||   | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |      |||| ||| |  ||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  ||||||||| ||||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||||  |||||  || |||||||  ||||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
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Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 12
US-10-252-518-5
; Sequence 5, Application US/10252518
; Patent No. 6875596
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Honma, Tsutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 03500.015225.2
; CURRENT APPLICATION NUMBER: US/10/252,518
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: JP 2000-095004
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word

; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
; FEATURE:
; FEATURE: cDNA to 16S rRNA
US-10-252-518-5

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

```
Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
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                ||||||||||||||||||||||||||| ||||||||||||||||||||| || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||   ||| ||||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              ||||||||||||||| |    |||||| |||||||||| |||||| |||||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| ||||| ||||||||||||||||||||||||| || ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              ||||||  |||||||||||   || |  | |||| |||  || |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              ||||||  |||  | ||||||||||||||| | |||||| ||||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | ||||||||||||| | ||| |||| ||| | |||| || | ||||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
                |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 13
US-08-114-695A-1
; Sequence 1, Application US/08114695A
; Patent No. 5508193
;  GENERAL INFORMATION:
;    APPLICANT:  Mandelbaum, Raphael T.
;    APPLICANT:  Wackett, Lawrence P.
;    TITLE OF INVENTION:  DEGRADATION OF S-TRIAZINES IN SOIL AND
;    TITLE OF INVENTION:  WATER
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCHWEGMAN, LUNDBERG & WOESSNER, P.A.
;      STREET:  3500 IDS CENTER
;      CITY:  MINNEAPOLIS
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/114,695A
;      FILING DATE:  31-AUG-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MUETING, ANN M.
;      REGISTRATION NUMBER:  33,977
;      REFERENCE/DOCKET NUMBER:  600.268US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-339-0331
;      TELEFAX:  612-339-3061
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1542 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  rRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Escherichia coli
US-08-114-695A-1

  Query Match             70.5%;  Score 1076;  DB 2;  Length 1542;
  Best Local Similarity   67.2%;  Pred. No. 0;
  Matches 1008;  Conservative  246;  Mismatches  243;  Indels    4;  Gaps    3;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGA--TAGCTTGCTATTAGGCG 87
              |||||||||| :||||||:|||||:||| ||| |||    ||   |||::||:  :  ||
Db         38 GGCGGCAGGCCTAACACATGCAAGTCGAACGGTAACACGGAAGAAGCTTGCTTCTTTGCT 97

Qy         88 TCGAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCG 147
                 | ||||||||:|||:||:   : |||| |: ||:  : | ||||||:| |:
Db         98 GACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTAC 157

Qy        148 GGGAAACTCGAATTAATACCGCATACGTCTACGGGAGAAAGCAGGGGNTCATTAGACCTT 207
              ||||||   | :||:||||||:|      | |   ||||  ||||  | :  | ||:
Db        158 UGGAAACGGUAGCUAAUACCGCAUAACGUCGCAGACCAAAGAGGGGGACCUUCGGGCCUC 217

Qy        208 GCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGC 267
              || |:  ||:| ||| |  : |||::|||:||  ||:||||:|| |||  |||  |||
Db        218 UUGCCAUCGGAUGUGCCCAGAUGGGAUUAGCUAGUAGGUGGGGUAACGGCUCACCUAGGC 277

Qy        268 GACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGG 327
              |||||:|  :|||:||:|:|||||||:|| |||||||||  || ||:|||||||||  || |
Db        278 GACGAUCCCUAGCUGGUCUGAGAGGAUGACCAGCCACACUGGAACUGAGACACGGUCCAG 337

Qy        328 ACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGGAACCCTGATCCAGCCA 386
              ||: |:|||||||||||||:||||||:|::| ||||:||  | || ||:||: ||||||
Db        338 ACUCCUACGGGAGGCAGCAGUGGGGAAUAUUGCACAAUGGGCGCAAGCCUGAUGCAGCCA 397

Qy        387 TGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTC 446
              :|||||:|: :|||||||||::  ||::|:|||| ||::: ||| | || ||||
Db        398 UGCCGCGUGUAUGAAGAAGGCCUUCGGGUUGUAAAGUACUUUCAGCGGGGAGGAAGGGAG 457

Qy        447 TTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTG 506
              :   |::||:|||    |  |  :||| ::| | |||||| ||||||||||:|||:| |:|
Db        458 UAAAGUUAAUACCUUUGCUCAUUGACGUUACCCGCAGAAGAAGCACCGGCUAACUCCGUG 517

Qy        507 CCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCG 566
              |||||||||||||:||:|| |||||:|||||||::||:|||||::||:|||||:||||||
Db        518 CCAGCAGCCGCGGUAAUACGGAGGGUGCAAGCGUUAAUCGGAAUUACUGGGCGUAAAGCG 577

Qy        567 AGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATC 626
              || ||| || ::| :|||:||||:|:|||||||||: ||||:||||||:|||:|||||:|
Db        578 CACGCAGGCGGUUUGUUAAGUCAGAUGUGAAAUCCCCGGGCUCAACCUGGGAACUGCAUC 637

Qy        627 TGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAAT 686
              :|| ||:|  | ||: |||:     ||||||  |:||||:: |||||:|:|||||:||||:
Db        638 UGAUACUGGCAAGCUUGAGUCUCGUAGAGGGGGGUAGAAUUCCAGGUGUAGCGGUGAAAU 697

Qy        687 GCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACT 746
              |||:|||||:|:| |||||:|||| :||||||||| ||  ||:||    | ||:||| |:
Db        698 GCGUAGAGAUCUGGAGGAAUACCGGUGGCGAAGGCGGCCCCCUGGACGAAGACUGACGCU 757

Qy        747 GAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC 806
              |||  |||||||||:||| ||||||||||::|||:||||:||:||:|||||||||:||||
Db        758 CAGGUGCGAAAGCGUGGGGAGCAAACAGGAUUAGAUACCCUGGUAGUCCACGCCGUAAAC 817

Qy        807 GATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAG 866
              ||:|:| ||: |  | : |  |||::|||| :   :  || |||:|||||  :|||: |
Db        818 GAUGUCGACUUGGAGGUUGUGCCCUUGAGGCGUGGCUUCCGGAGCUAACGCGUUAAGUCG 877

Qy        867 ACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACA 926
              ||||||:||||||:|||||||||||::|||||:||||:|||::|||||||||||||||||
```

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Db        878 ACCGCCUGGGGAGUACGGCCGCAAGGUUAAAACUCAAAUGAAUUGACGGGGGCCCGCACA 937

Qy        927 AGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACAT 986

Db        938 AGCGGUGGAGCAUGUGGUUUAAUUCGAUGCAACGCGAAGAACCUUACCUGGUCUUGACAU 997

Qy        987 ACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATG 1046

Db        998 CCACGGAAGUUUUCAGAGAUGAGAAUGUGCCUUCGGGAACCGUGAGACAGGUGCUGCAUG 1057

Qy       1047 GCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTG 1106

Db       1058 GCUGUCGUCAGCUCGUGUUGUGAAAUGUUGGGUUAAGUCCCGCAACGAGCGCAACCCUUA 1117

Qy       1107 TCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1118 UCCUUUGUUGCCAGCGGUCCGGCCGGGAACUCAAAGGAGACUGCCAGUGAUAAACUGGAG 1177

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1178 GAAGGUGGGGAUGACGUCAAGUCAUCAUGGCCCUUACGACCAGGGCUACACACGUGCUAC 1237

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1238 AAUGGCGCAUACAAAGAGAAGCGACCUCGCGAGAGCAAGCGGACCUCAUAAAGUGCGUCG 1297

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1298 UAGUCCGGAUUGGAGUCUGCAACUCGACUCCAUGAAGUCGGAAUCGCUAGUAAUCGUGGA 1357

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1358 UCAGAAUGCCACGGUGAAUACGUUCCCGGGCCUUGUACACACCGCCCGUCACACCAUGGG 1417

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1418 AGUGGGUUGCAAAAGAAGUAGGUAGCUUAACCUUCGGGAGGGCGCUUACCACUUUGUGAU 1477

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCT 1525

Db       1478 UCAUGACUGGGGUGAAGUCGUAACAAGGUAACCGUAGGGGAACCUGCGGUUGGAUCACCU 1537

Qy       1526 C 1526

Db       1538 C 1538


RESULT 14
US-09-737-297-4
; Sequence 4, Application US/09737297
; Patent No. 6887984
; GENERAL INFORMATION:
;  APPLICANT: Berry, Mark
;  APPLICANT:  Griffiths, Allen
;  APPLICANT:  Hill, Philip
;  APPLICANT:  Laybourne-Parry, Johanna
;  APPLICANT:  Mills, Sarah
;  TITLE OF INVENTION: Processes and Organisms for the Production of Antifreeze Proteins
;  FILE REFERENCE: F3247
;  CURRENT APPLICATION NUMBER: US/09/737,297
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: GB 9929696.4
;  PRIOR FILING DATE: 1999-12-15
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 1481
;   TYPE: DNA
;   ORGANISM: Marinomonas communis
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (203)..(204)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (840)..(840)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (964)..(965)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (1142)..(1142)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (1182)..(1182)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (1185)..(1186)
;   OTHER INFORMATION: base identity unsure
;   NAME/KEY: Unsure
;   LOCATION: (1449)..(1449)
;   OTHER INFORMATION: base identity unsure
US-09-737-297-4

  Query Match             70.4%;  Score 1073.8;  DB 3;  Length 1481;
  Best Local Similarity   86.0%;  Pred. No. 0;
  Matches 1242;  Conservative    0;  Mismatches  198;  Indels    5;  Gaps    5;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db         39 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGTAACATTGCTAGCTTGCTAGAAGATGAC 98

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         99 GAGCGG-CGGACGGGTGAGTAACGCGTAGGAATCTGCCTAGTAGTGGGGGACAACATGTG 157

Qy        150 GAAACTCGAATTAATACCGCATACG-TCTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        158 GAAACGCATGCTAATACCGCATACGCCCTACGGGGGAAAGGAGGGNNTCTTCGGACCTTT 217

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        218 CGCTATTAGATGAGCCTGCGTGAGATTAGCTAGTTGGTGGGGTAAAGGCCTACCAAGGCG 277

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        278 ACGATCTCTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGA 337

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        338 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGCAAGCCTGATCCAGCCAT 397

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        398 GCCGCGTGTGTGAAGAAGGCCTTAGGGTTGTAAAGCACTTTCAGGAGTGAGGAAGGGCGT 457

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        458 ATAGTTAATACCTGTATGTTTTGACGTTAACTCCAGAAGAAGCACCGGCTAACTCTGTGC 517

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        518 CAGCAGCCGCGGTAATACAGAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 577

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        578 GCGTAGGCGGTTTGTTAAGTCGGATGTGAAATCCCAGGGCTCAACCTTGGAATGGCACCC 637

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        638 GATACTGGCAGGCTAGAGTACGGTAGAGGGGTGTGGAATTTCCTGTGTAGCGGTGAAATG 697

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
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Db        698 CGTAGATATAGGAAGGAACATCAGTGGCGAAGGCGACACCCTGGACCGATACTGACGCTG 757

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              ||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        758 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 817

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              |||||||||| |||||||     |      |||||| |||||||||||| |||||||||
Db        818 ATGTCTACTAGCCGTTGGG-GATNTATTTCTTTAGTGGCGCAGCTAACGCGATAAGTAGA 876

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 936

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||||   |||||||||||||||||| ||||||||||
Db        937 GCGGTGGAGCATGTGGTTTAATTCGAANNAACGCGAAGAACCTTACCTACTCTTGACATC 996

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              || ||||  ||  ||||||      |||||||||||| | ||| ||||||||||||||||
Db        997 CAGAGAACTTTYCAGAGATGAATTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGG 1056

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              |||||||||||||||| |||| ||||||||||||||||| |||||||||||||||| |
Db       1057 CTGTCGTCAGCTCGTGTTGTGAAATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTAT 1116

Qy       1108 CCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAGG 1167
              ||||| || |||||||||||||| |||||||||| |||||| ||||||||| |||||
Db       1117 CCTTATTTGCCAGCACTTCGGGTGGNAACTCTAAGGAGACTGCCGGTGACAAACCGGAGG 1176

Qy       1168 AAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACA 1227
              ||||  ||  |||||||||||||||||||||||||||  ||||||||||||||||||||
Db       1177 AAGGTNGGNNCGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACA 1236

Qy       1228 ATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCGT 1287
              ||||    |||||||||||||| |    |||| |  | || |||| |||||||    ||||
Db       1237 ATGGCGTATACAGAGGGCAGCGAACTCGCGAGGGTAAGCAAATCCCAAAAAGTACGTCGT 1296

Qy       1288 AGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGAT 1347
              ||||| |||||||||||||||||||||||||||||||||| |||||||||||||||| | ||
Db       1297 AGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGAAT 1356

Qy       1348 CAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGA 1407
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1357 CAGAATGTCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGA 1416

Qy       1408 GTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGTC 1466
              ||||||||| |||||||| | |||| ||| ||  | || |||| | ||||||| ||||||
Db       1417 GTTGATTGCTCCAGAAGTAGCTAGCTTAACCTNCGGGATGGCGGTTACCACGGAGTGGTC 1476

Qy       1467 GATGA 1471
                |||||
Db       1477 AATGA 1481


RESULT 15
US-09-726-774-3
; Sequence 3, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/09/726,774
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1467
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-726-774-3

  Query Match            70.2%;  Score 1070.8;  DB 3;  Length 1467;
  Best Local Similarity  85.9%;  Pred. No. 0;
  Matches 1233;  Conservative    0;  Mismatches  199;  Indels    4;  Gaps    4;

Qy         95 GCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGGGAAAC 154
              | |||||||||||||||| | ||||||||| |||  |||||||||| | |      ||||
Db         29 GGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGATAGTGGGGGACAACGTTTCGAAAG 88

Qy        155 TCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTGCGCTA 213
                  |||||||||||||||| |||||||||||||||||||  | |  | ||||||||||
Db         89 GAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTGCGCTA 148

Qy        214 TTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCGACGAT 273
              | |||||||||| |||||||||||||| ||||| ||||| |||  |||| |||||||||
Db        149 TCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGAT 208

Qy        274 CTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGACT-CT 332
              | ||| |||||||||||||||||||||| ||||| || |||||||||||| || |||| ||
Db        209 CCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCT 268

Qy        333 ACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCATGCCGC 392
              |||||||||||||||||||||||||||||||||  | || ||||||||||||||||||
Db        269 ACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGC 328

Qy        393 GTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCTTCGGT 452
              |||||||||||||| ||| | |||||||||||||||  | || ||||    ||
Db        329 GTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCATTAACC 388

Qy        453 TAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGCCAGCA 512
              ||||||    |      |||| ||| |  ||||||||||||||||||||  |||||||||
Db        389 TAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTTCGTGCCAGCA 448

Qy        513 GCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGTA 572
              |||||||||||||  |||||||||||||||||||||||||||||||||||||| |||||
Db        449 GCCGCGGTAATACGAAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTA 508

Qy        573 GGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCTGAAAC 632
              ||||| ||| |||||   |||||||| |||||||| |||||||||||||||  ||||
Db        509 GGTGGTTTGTTAAGTTGAATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAAC 568

Qy        633 TGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATGCGTAG 692
              ||  | |||||||| |  ||||||  || |||||||  |||||||||||||||||||||
Db        569 TGGCAAGCTAGAGTATGGCAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAG 628

Qy        693 AGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTGAGGCT 752
              | ||  |||||||  |||  |||||||||  |  |||||  | ||||||||||||||||
Db        629 ATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGGCTAATACTGACACTGAGGTG 688

Qy        753 CGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTC 812
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        689 CGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTC 748

Qy        813 TACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGACCGCC 872
              |||||  |||||||  |||||||  |||||||  |||||||||||||  |||||  |||||||
Db        749 GACTAGCCGTTGGGATCCTTGAGATCTTAGTGGCGCAGCTAACGCATTAAGTCGACCGCC 808

Qy        873 TGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGT 932
              |||||||||||||||  |||||||||||  ||||||||||||||||||||||||||||||
Db        809 TGGGGAGTACGGCCGCTAGGTTAAAACTCTAATGAATTGACGGGGGCCCGCACAAGCGGT 868

Qy        933 GGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATACACAG 992
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||| || ||
Db        869 GGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATGCAGAG 928

Qy        993 AATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGGCTGTC 1052
              ||  ||  ||||||      |||||||||||||| | ||| ||||||||||||||||||||
Db        929 AACTTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGACACAGGTGCTGCATGGCTGTC 988

Qy       1053 GTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCTTA 1112
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Db        989 GTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGTCCTTA 1048

Qy       1113 GTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAGGAAGG 1171
              ||||||||||| ||  |||||| |||||||||| |||||| ||||||||| |||||||||
Db       1049 GTTACCAGCACGTTAAGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAGGAAGG 1108

Qy       1172 CGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGG 1231
              |||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Db       1109 TGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTACAATGG 1168

Qy       1232 TAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCGTAGTC 1291
              | |||||| ||||  || |  | |||| |||  || |||| || ||| || |||||||||
Db       1169 TCGGTACAAAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCATAAAACCGATCGTAGTC 1228

Qy       1292 CAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGATCAGA 1351
              | ||| | |||||||||||||||| | |||||| |||||||||||||||| | ||||||
Db       1229 CGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGTGAATCAGA 1288

Qy       1352 ATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTTG 1411
              ||| | ||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1289 ATGTCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGG 1348

Qy       1412 ATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGTCGATG 1470
              |||| |||||||| | ||| |||| ||| | | || || | ||||||| |   |  |||
Db       1349 GTTGCTCCAGAAGTAGCTAGTCTAACCTTCGGGGGGACGGTTACCACGGAGGTATTCATG 1408

Qy       1471 ACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCTC 1526
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1409 ACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCACCTC 1464
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Job time : 350.745 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 2, 2005, 23:29:37 ; Search time 20.156 Seconds
(without alignments)
7795.112 Million cell updates/sec

Title: US-09-979-558A-2
Perfect score: 19
Sequence: 1 taatgtcatcgtccccggg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	16.4	86.3	1329	7	US-10-169-395-18	Sequence 18, Appl
2	16.4	86.3	1400	9	US-10-956-157-7824	Sequence 7824, Ap
3	16.4	86.3	1400	9	US-10-956-157-9435	Sequence 9435, Ap
4	16.4	86.3	1882	3	US-09-925-298-301	Sequence 301, App
5	16.4	86.3	1882	5	US-10-102-806-301	Sequence 301, App
6	16.4	86.3	1926	3	US-09-764-853-238	Sequence 238, App
7	16.4	86.3	1987	3	US-09-818-143-20	Sequence 20, Appl
8	16.4	86.3	1989	3	US-09-946-374-76	Sequence 76, Appl
9	16.4	86.3	1989	5	US-10-006-856A-76	Sequence 76, Appl
10	16.4	86.3	1989	5	US-10-006-818A-76	Sequence 76, Appl
11	16.4	86.3	1989	5	US-10-006-485A-76	Sequence 76, Appl
12	16.4	86.3	1989	5	US-10-013-907A-76	Sequence 76, Appl
13	16.4	86.3	1989	5	US-10-015-499A-76	Sequence 76, Appl
14	16.4	86.3	1989	5	US-10-015-393A-76	Sequence 76, Appl
15	16.4	86.3	1989	5	US-10-015-869A-76	Sequence 76, Appl
16	16.4	86.3	1989	5	US-10-012-121A-76	Sequence 76, Appl
17	16.4	86.3	1989	5	US-10-006-116A-76	Sequence 76, Appl
18	16.4	86.3	1989	5	US-10-006-117A-76	Sequence 76, Appl
19	16.4	86.3	1989	5	US-10-017-527A-76	Sequence 76, Appl
20	16.4	86.3	1989	5	US-10-013-913A-76	Sequence 76, Appl
21	16.4	86.3	1989	5	US-10-007-194A-76	Sequence 76, Appl
22	16.4	86.3	1989	5	US-10-013-430A-76	Sequence 76, Appl
23	16.4	86.3	1989	5	US-10-011-671A-76	Sequence 76, Appl
24	16.4	86.3	1989	5	US-10-012-755A-76	Sequence 76, Appl
25	16.4	86.3	1989	5	US-10-015-386A-76	Sequence 76, Appl
26	16.4	86.3	1989	5	US-10-011-692A-76	Sequence 76, Appl
27	16.4	86.3	1989	5	US-10-006-768A-76	Sequence 76, Appl
28	16.4	86.3	1989	5	US-10-017-610A-76	Sequence 76, Appl
29	16.4	86.3	1989	5	US-10-006-063A-76	Sequence 76, Appl
30	16.4	86.3	1989	6	US-10-020-063A-76	Sequence 76, Appl
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32	16.4	86.3	1989	6	US-10-017-407A-76	Sequence 76, Appl
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35	16.4	86.3	1989	6	US-10-015-822A-76	Sequence 76, Appl
36	16.4	86.3	1989	6	US-10-015-387A-76	Sequence 76, Appl
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40	16.4	86.3	1989	6	US-10-015-392A-76	Sequence 76, Appl
41	16.4	86.3	1989	6	US-10-017-306A-76	Sequence 76, Appl
42	16.4	86.3	1989	6	US-10-017-867A-76	Sequence 76, Appl
43	16.4	86.3	1989	6	US-10-012-064A-76	Sequence 76, Appl
44	16.4	86.3	1989	6	US-10-013-909A-76	Sequence 76, Appl
45	16.4	86.3	1989	6	US-10-015-671A-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-10-169-395-18
; Sequence 18, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING
; TITLE OF INVENTION: THESE PROTEINS
; FILE REFERENCE: 01997.015100.US
; CURRENT APPLICATION NUMBER: US/10/169,395
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/JP00/09359
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 150
; SEQ ID NO 18
; LENGTH: 1329
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-169-395-18

Query Match 86.3%; Score 16.4; DB 7; Length 1329;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
US-10-956-157-7824
; Sequence 7824, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

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;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7824
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-956-157-7824

  Query Match             86.3%;  Score 16.4;  DB 9;  Length 1400;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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US-10-956-157-9435
; Sequence 9435, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William
;  TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
;  TITLE OF INVENTION:  HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
;  FILE REFERENCE: 031896-043000 (AM 101081)
;  CURRENT APPLICATION NUMBER: US/10/956,157
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 319805
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9435
;   LENGTH: 1400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-956-157-9435

  Query Match             86.3%;  Score 16.4;  DB 9;  Length 1400;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 4
US-09-925-298-301
; Sequence 301, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103
;  CURRENT APPLICATION NUMBER: US/09/925,298
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
;   LENGTH: 1882
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (22)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (223)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1840)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1849)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-298-301

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 1882;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
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Db        529 AATGTCATCGTCCCCGAG 546


RESULT 5
US-10-102-806-301
; Sequence 301, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 301
;   LENGTH: 1882
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (22)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (223)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1840)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (1849)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-301

  Query Match             86.3%;  Score 16.4;  DB 5;  Length 1882;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
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RESULT 6
US-09-764-853-238
; Sequence 238, Application US/09764853
; Patent No. US20020090672A1
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; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ06
;  CURRENT APPLICATION NUMBER: US/09/764,853
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 939
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
;   LENGTH: 1926
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-853-238

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RESULT 7
US-09-818-143-20
; Sequence 20, Application US/09818143
; Patent No. US20020019000A1
; GENERAL INFORMATION:
;  APPLICANT: Walker, Michael G.
;  APPLICANT:  Volkmuth, Wayne
;  APPLICANT:  Klingler, Tod M.
;  TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
;  FILE REFERENCE: PB-0004 CIP
;  CURRENT APPLICATION NUMBER: US/09/818,143
;  CURRENT FILING DATE:  2001-03-26
;  NUMBER OF SEQ ID NOS: 23
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;   ORGANISM: Homo sapiens
;   FEATURE: -
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US-09-818-143-20

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 1987;
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  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
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RESULT 8
US-09-946-374-76
; Sequence 76, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C1
;  CURRENT APPLICATION NUMBER: US/09/946,374
;  CURRENT FILING DATE:  2001-09-04
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/105266
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; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 86.3%; Score 16.4; DB 3; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        715 AATGTCATCGTCCCCGAG 732
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RESULT 9
US-10-006-856A-76
; Sequence 76, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477

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;  Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 76
;   LENGTH: 1989
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-006-856A-76

  Query Match             86.3%;  Score 16.4;  DB 5;  Length 1989;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              ||||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732


RESULT 10
US-10-006-818A-76
; Sequence 76, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C4
;  CURRENT APPLICATION NUMBER: US/10/006,818A
;  CURRENT FILING DATE:  2001-12-06
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
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;   LENGTH: 1989
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-006-818A-76

  Query Match             86.3%;  Score 16.4;  DB 5;  Length 1989;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+02;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              ||||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732


RESULT 11
US-10-006-485A-76
; Sequence 76, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C9
;  CURRENT APPLICATION NUMBER: US/10/006,485A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098750
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098821
;  PRIOR FILING DATE: 1998-09-02
;  PRIOR APPLICATION NUMBER: 60/098843
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;  PRIOR FILING DATE: 1998-09-09
;  PRIOR APPLICATION NUMBER: 60/099598
;  PRIOR FILING DATE: 1998-09-09
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;  PRIOR FILING DATE: 1998-09-09
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;  PRIOR APPLICATION NUMBER: 60/100388
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100390
;  PRIOR FILING DATE: 1998-09-15
;  PRIOR APPLICATION NUMBER: 60/100584
;  PRIOR FILING DATE: 1998-09-16
;  PRIOR APPLICATION NUMBER: 60/100627
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;  PRIOR APPLICATION NUMBER: 60/100848
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; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
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; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
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; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
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; PRIOR FILING DATE: 1998-10-08
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; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 86.3%; Score 16.4; DB 5; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 AATGTCATCGTCCCCGGG 19
              ||||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732
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RESULT 12
US-10-013-907A-76
; Sequence 76, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A

; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-013-907A-76

Query Match 86.3%; Score 16.4; DB 5; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||||||||||| |
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 13
US-10-015-499A-76
; Sequence 76, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-499A-76

Query Match 86.3%; Score 16.4; DB 5; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||||||||||| |
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 14
US-10-015-393A-76
; Sequence 76, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-393A-76

Query Match 86.3%; Score 16.4; DB 5; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
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Db 715 AATGTCATCGTCCCCGAG 732

RESULT 15
US-10-015-869A-76
; Sequence 76, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-869A-76

Query Match 86.3%; Score 16.4; DB 5; Length 1989;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
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Db 715 AATGTCATCGTCCCCGAG 732

Search completed: December 3, 2005, 03:22:27
Job time : 21.156 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 2, 2005, 23:40:24 ; Search time 3.17282 Seconds
(without alignments)
1863.702 Million cell updates/sec

Title: US-09-979-558A-2
Perfect score: 19
Sequence: 1 taatgtcatcgtccccggg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	14.8	77.9	991	6	US-10-750-185-30544	Sequence 30544, A
c	3	14.8	77.9	1323	6	US-10-821-234-430	Sequence 430, App
	4	14.8	77.9	1462	6	US-10-750-185-45402	Sequence 45402, A
c	5	14.4	75.8	19	8	US-11-101-244-1513769	Sequence 1513769,
c	6	14.4	75.8	19	8	US-11-101-244-1513798	Sequence 1513798,
c	7	14.4	75.8	19	9	US-11-083-784-1513769	Sequence 1513769,
c	8	14.4	75.8	19	9	US-11-083-784-1513798	Sequence 1513798,
	9	14.4	75.8	1131	6	US-10-750-185-29301	Sequence 29301, A
	10	14.2	74.7	1224	6	US-10-750-185-26730	Sequence 26730, A
	11	14.2	74.7	1744	6	US-10-750-185-27275	Sequence 27275, A
c	12	14.2	74.7	3176	6	US-10-750-185-43645	Sequence 43645, A
	13	14.2	74.7	155515	7	US-11-112-908-42	Sequence 42, Appl
	14	14.2	74.7	159660	7	US-11-112-908-43	Sequence 43, Appl
	15	14.2	74.7	177623	7	US-11-112-908-41	Sequence 41, Appl
	16	14	73.7	1799	6	US-10-750-185-56513	Sequence 56513, A
c	17	13.8	72.6	19	8	US-11-101-244-183098	Sequence 183098,
c	18	13.8	72.6	19	9	US-11-083-784-183098	Sequence 183098,
	19	13.8	72.6	717	6	US-10-467-657-5135	Sequence 5135, Ap
c	20	13.8	72.6	762	6	US-10-467-657-5137	Sequence 5137, Ap
c	21	13.8	72.6	1411	6	US-10-750-185-36853	Sequence 36853, A
	22	13.8	72.6	1806	6	US-10-131-826A-121	Sequence 121, App
	23	13.8	72.6	2292	6	US-10-821-234-168	Sequence 168, App
	24	13.8	72.6	3055	7	US-11-102-217-26	Sequence 26, Appl
c	25	13.8	72.6	3532	6	US-10-750-185-51277	Sequence 51277, A
	26	13.8	72.6	5034	7	US-11-102-217-30	Sequence 30, Appl
	27	13.8	72.6	5483	7	US-11-102-217-38	Sequence 38, Appl
	28	13.8	72.6	6071	7	US-11-102-217-29	Sequence 29, Appl
	29	13.8	72.6	7926	7	US-11-102-217-53	Sequence 53, Appl
	30	13.8	72.6	8499	7	US-11-102-217-37	Sequence 37, Appl
	31	13.4	70.5	19	8	US-11-101-244-49886	Sequence 49886, A
	32	13.4	70.5	19	9	US-11-083-784-49886	Sequence 49886, A
c	33	13.4	70.5	1146	6	US-10-858-730-171	Sequence 171, App
c	34	13.4	70.5	16382	7	US-11-108-172-1112	Sequence 1112, Ap
c	35	13.2	69.5	19	8	US-11-101-244-1282003	Sequence 1282003,
c	36	13.2	69.5	19	9	US-11-083-784-1282003	Sequence 1282003,
c	37	13.2	69.5	552	7	US-11-074-176-15	Sequence 15, Appl
	38	13.2	69.5	600	6	US-10-750-185-20926	Sequence 20926, A
c	39	13.2	69.5	936	6	US-10-750-185-37279	Sequence 37279, A
	40	13.2	69.5	1158	6	US-10-392-234A-27	Sequence 27, Appl
	41	13.2	69.5	1212	6	US-10-858-730-55	Sequence 55, Appl
c	42	13.2	69.5	1448	6	US-10-750-185-46298	Sequence 46298, A
c	43	13.2	69.5	1534	6	US-10-750-185-62976	Sequence 62976, A
c	44	13.2	69.5	1594	6	US-10-750-185-43137	Sequence 43137, A
	45	13.2	69.5	1648	6	US-10-750-185-59897	Sequence 59897, A

ALIGNMENTS

RESULT 1
US-10-750-185-61069
; Sequence 61069, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 61069
; LENGTH: 1042
; TYPE: DNA
; ORGANISM: Bovine 19866881140809
US-10-750-185-61069

Query Match 81.1%; Score 15.4; DB 6; Length 1042;
Best Local Similarity 94.1%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TAATGTCATCGTCCCCG 17
              |||||||||| ||||||
Db        900 TAATGTCATCTTCCCCG 916
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RESULT 2
US-10-750-185-30544/c
; Sequence 30544, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 30544
; LENGTH: 991
; TYPE: DNA
; ORGANISM: Bovine 19866881165598
US-10-750-185-30544

Query Match 77.9%; Score 14.8; DB 6; Length 991;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||| ||| ||||
Db 731 AATGTCATCTTCCACGGG 714

RESULT 3
US-10-821-234-430/c
; Sequence 430, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 430
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-430

Query Match 77.9%; Score 14.8; DB 6; Length 1323;
Best Local Similarity 88.9%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||| ||| ||||
Db 1275 AATGTCATCCTCCACGGG 1258

RESULT 4
US-10-750-185-45402
; Sequence 45402, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 45402
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Bovine 19866880900426
US-10-750-185-45402

Query Match 77.9%; Score 14.8; DB 6; Length 1462;
Best Local Similarity 88.9%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TAATGTCATCGTCCCCGG 18
|||||||| ||||||||
Db 1274 TAATGTCAATGTCCCCGG 1291

RESULT 5
US-11-101-244-1513769/c
; Sequence 1513769, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513769
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1513769

Query Match 75.8%; Score 14.4; DB 8; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCG 17
|||||||||||||| ||
Db 19 AATGTCATCGTCCTCG 4

RESULT 6
US-11-101-244-1513798/c
; Sequence 1513798, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513798
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1513798

Query Match 75.8%; Score 14.4; DB 8; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCG 17
||||||||||||| ||
Db 16 AATGTCATCGTCCTCG 1

RESULT 7
US-11-083-784-1513769/c
; Sequence 1513769, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513769
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1513769

Query Match 75.8%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCG 17
||||||||||||| ||
Db 19 AATGTCATCGTCCTCG 4

RESULT 8
US-11-083-784-1513798/c
; Sequence 1513798, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1513798
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1513798

Query Match 75.8%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCG 17
||||||||||||| ||
Db 16 AATGTCATCGTCCTCG 1

RESULT 9
US-10-750-185-29301
; Sequence 29301, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 29301
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Bovine 19866881234047
US-10-750-185-29301

Query Match 75.8%; Score 14.4; DB 6; Length 1131;
Best Local Similarity 93.8%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGTCATCGTCCCCGGG 19
|||||| |||||||||
Db 110 TGTCATTGTCCCCGGG 125

RESULT 10
US-10-750-185-26730
; Sequence 26730, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

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;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 26730
;   LENGTH: 1224
;   TYPE: DNA
;   ORGANISM: Bovine  19866881201331
US-10-750-185-26730

  Query Match             74.7%;  Score 14.2;  DB 6;  Length 1224;
  Best Local Similarity   84.2%;  Pred. No. 1.7e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAATGTCATCGTCCCCGGG 19
              |||||||||  |||| |||
Db        374 TAATGTCATTCTCCCAGGG 392


RESULT 11
US-10-750-185-27275
; Sequence 27275, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 27275
;   LENGTH: 1744
;   TYPE: DNA
;   ORGANISM: Bovine  19866880624605
US-10-750-185-27275

  Query Match             74.7%;  Score 14.2;  DB 6;  Length 1744;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAATGTCATCGTCCCCGGG 19
              || |||||||||| | |||
Db       1089 TACTGTCATCGTCACTGGG 1107


RESULT 12
US-10-750-185-43645/c
; Sequence 43645, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 43645
;   LENGTH: 3176
;   TYPE: DNA
;   ORGANISM: Bovine  19866880681516
US-10-750-185-43645

  Query Match             74.7%;  Score 14.2;  DB 6;  Length 3176;
  Best Local Similarity   84.2%;  Pred. No. 1.8e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAATGTCATCGTCCCCGGG 19
              | ||||||| ||||||  ||
Db        172 TCATGTCATTGTCCCCTGG 154


RESULT 13
US-11-112-908-42
; Sequence 42, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
;   LENGTH: 155515
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-42

  Query Match             74.7%;  Score 14.2;  DB 7;  Length 155515;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAATGTCATCGTCCCCGGG 19
              ||||| ||||||||  |||
Db     101533 TAATGCCATCGTCCTGGGG 101551


RESULT 14
US-11-112-908-43
; Sequence 43, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
;   LENGTH: 159660
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-43

  Query Match             74.7%;  Score 14.2;  DB 7;  Length 159660;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAATGTCATCGTCCCCGGG 19
              ||||| |||||||| |||
Db      91336 TAATGCCATCGTCCTGGGG 91354


RESULT 15
US-11-112-908-41
; Sequence 41, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
;   LENGTH: 177623
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-41

  Query Match             74.7%;  Score 14.2;  DB 7;  Length 177623;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAATGTCATCGTCCCCGGG 19
              ||||| |||||||| |||
Db     159600 TAATGCCATCGTCCTGGGG 159618


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
7937.378 Million cell updates/sec

Title: US-09-979-558A-2
Perfect score: 19
Sequence: 1 taatgtcatcgtccccggg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.4	86.3	1989	3	US-10-012-231A-76	Sequence 76, Appl
	2	16.4	86.3	1989	3	US-10-015-389A-76	Sequence 76, Appl
	3	16.4	86.3	1989	3	US-10-006-768A-76	Sequence 76, Appl
	4	16.4	86.3	1989	3	US-10-015-671A-76	Sequence 76, Appl
	5	16.4	86.3	1989	3	US-10-015-393A-76	Sequence 76, Appl
	6	16.4	86.3	1989	3	US-10-011-833A-76	Sequence 76, Appl
	7	16.4	86.3	1989	3	US-10-006-041A-76	Sequence 76, Appl
	8	16.4	86.3	1989	3	US-10-012-064A-76	Sequence 76, Appl
	9	16.4	86.3	2132	3	US-09-552-322-1	Sequence 1, Appli
c	10	15.4	81.1	597	4	US-09-605-703B-2881	Sequence 2881, Ap
	11	15.4	81.1	601	3	US-09-949-016-136302	Sequence 136302,
c	12	15.4	81.1	2338	3	US-09-582-337-1	Sequence 1, Appli
c	13	15.4	81.1	2350	3	US-09-187-478-1	Sequence 1, Appli
c	14	15.4	81.1	2350	3	US-09-292-036-1	Sequence 1, Appli
c	15	15.4	81.1	51049	3	US-09-949-016-15571	Sequence 15571, A
c	16	15	78.9	636	3	US-09-902-540-8517	Sequence 8517, Ap
c	17	15	78.9	6855	3	US-09-902-540-897	Sequence 897, App
	18	14.8	77.9	99	2	US-08-427-097-12	Sequence 12, Appl
	19	14.8	77.9	99	2	US-08-878-957-12	Sequence 12, Appl
c	20	14.8	77.9	170	2	US-08-419-078-5	Sequence 5, Appli
c	21	14.8	77.9	170	2	US-08-419-078-6	Sequence 6, Appli
c	22	14.8	77.9	170	2	US-08-726-883-5	Sequence 5, Appli
c	23	14.8	77.9	170	2	US-08-726-883-6	Sequence 6, Appli
c	24	14.8	77.9	300	2	US-08-419-078-4	Sequence 4, Appli
c	25	14.8	77.9	300	2	US-08-726-883-4	Sequence 4, Appli
	26	14.8	77.9	384	3	US-09-389-681-451	Sequence 451, App
	27	14.8	77.9	384	3	US-09-620-405B-451	Sequence 451, App
	28	14.8	77.9	384	3	US-09-433-826B-451	Sequence 451, App
	29	14.8	77.9	384	3	US-09-604-287A-451	Sequence 451, App
	30	14.8	77.9	384	3	US-09-834-759-451	Sequence 451, App
	31	14.8	77.9	384	3	US-09-590-751A-451	Sequence 451, App
	32	14.8	77.9	384	3	US-09-551-621-451	Sequence 451, App
	33	14.8	77.9	384	3	US-09-551-621A-451	Sequence 451, App
	34	14.8	77.9	384	3	US-10-076-622-451	Sequence 451, App
	35	14.8	77.9	686	3	US-09-533-559-6102	Sequence 6102, Ap
c	36	14.8	77.9	879	3	US-09-248-796A-7856	Sequence 7856, Ap
c	37	14.8	77.9	1022	3	US-10-002-344A-48	Sequence 48, Appl
c	38	14.8	77.9	1322	2	US-08-419-078-1	Sequence 1, Appli
c	39	14.8	77.9	1322	2	US-08-726-883-1	Sequence 1, Appli
c	40	14.8	77.9	1323	3	US-09-023-655-55	Sequence 55, Appl
c	41	14.8	77.9	1594	3	US-09-270-767-14907	Sequence 14907, A
	42	14.8	77.9	1752	2	US-08-427-097-13	Sequence 13, Appl
	43	14.8	77.9	1752	2	US-08-427-097-19	Sequence 19, Appl
	44	14.8	77.9	1752	2	US-08-878-957-13	Sequence 13, Appl
	45	14.8	77.9	1752	2	US-08-878-957-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-012-231A-76
; Sequence 76, Application US/10012231A
; Patent No. 6924355
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-231A-76

Query Match 86.3%; Score 16.4; DB 3; Length 1989;
Best Local Similarity 94.4%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 AATGTCATCGTCCCCGGG 19
              ||||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732
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RESULT 2
US-10-015-389A-76
; Sequence 76, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C48
;  CURRENT APPLICATION NUMBER: US/10/015,389A
;  CURRENT FILING DATE:  2002-06-25
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
;   LENGTH: 1989
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-389A-76

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 1989;
  Best Local Similarity   94.4%;  Pred. No. 97;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              |||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732


RESULT 3
US-10-006-768A-76
; Sequence 76, Application US/10006768A
; Patent No. 6936697
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C10
;  CURRENT APPLICATION NUMBER: US/10/006,768A
;  CURRENT FILING DATE:  2002-03-05
;  NUMBER OF SEQ ID NOS: 477
;  Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 76
;   LENGTH: 1989
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-006-768A-76

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 1989;
  Best Local Similarity   94.4%;  Pred. No. 97;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              |||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732


RESULT 4
US-10-015-671A-76
; Sequence 76, Application US/10015671A
; Patent No. 6946263
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C47
;  CURRENT APPLICATION NUMBER: US/10/015,671A
;  CURRENT FILING DATE:  2001-12-11
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
;   LENGTH: 1989
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-671A-76

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 1989;
  Best Local Similarity   94.4%;  Pred. No. 97;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              |||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732


RESULT 5
US-10-015-393A-76
; Sequence 76, Application US/10015393A
; Patent No. 6951737
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C46
;  CURRENT APPLICATION NUMBER: US/10/015,393A
;  CURRENT FILING DATE:  2002-06-10
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
;   LENGTH: 1989
;   TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-015-393A-76

Query Match 86.3%; Score 16.4; DB 3; Length 1989;
Best Local Similarity 94.4%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||||||||| |
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 6
US-10-011-833A-76
; Sequence 76, Application US/10011833A
; Patent No. 6951920
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-011-833A-76

Query Match 86.3%; Score 16.4; DB 3; Length 1989;
Best Local Similarity 94.4%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||||||||| |
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 7
US-10-006-041A-76
; Sequence 76, Application US/10006041A
; Patent No. 6951921
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-041A-76

Query Match 86.3%; Score 16.4; DB 3; Length 1989;
Best Local Similarity 94.4%; Pred. No. 97;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AATGTCATCGTCCCCGGG 19
||||||||||||||| |
Db 715 AATGTCATCGTCCCCGAG 732

RESULT 8
US-10-012-064A-76
; Sequence 76, Application US/10012064A
; Patent No. 6953841
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 76
; LENGTH: 1989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-064A-76

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  Query Match             86.3%;  Score 16.4;  DB 3;  Length 1989;
  Best Local Similarity   94.4%;  Pred. No. 97;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              |||||||||||||||| |
Db        715 AATGTCATCGTCCCCGAG 732


RESULT 9
US-09-552-322-1
; Sequence 1, Application US/09552322
; Patent No. 6436642
; GENERAL INFORMATION:
;  APPLICANT: Gould-Rothberg
;  APPLICANT:  Rastelli
;  TITLE OF INVENTION: METHOD OF CLASSIFYING A THYROID CARCINOMA USING
;  TITLE OF INVENTION:  DIFFERENTIAL GENE EXPRESSION
;  FILE REFERENCE: 15966-548
;  CURRENT APPLICATION NUMBER: US/09/552,322
;  CURRENT FILING DATE:  2000-04-19
;  PRIOR APPLICATION NUMBER: 60/130,123
;  PRIOR FILING DATE: 1999-04-20
;  PRIOR APPLICATION NUMBER: 60/193,203
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2132
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-552-322-1

  Query Match             86.3%;  Score 16.4;  DB 3;  Length 2132;
  Best Local Similarity   94.4%;  Pred. No. 98;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGGG 19
              |||||||||||||||| |
Db        844 AATGTCATCGTCCCCGAG 861


RESULT 10
US-09-605-703B-2881/c
; Sequence 2881, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: BGI-129CP
;  CURRENT APPLICATION NUMBER: US/09/605,703B
;  CURRENT FILING DATE:  2000-06-27
;  PRIOR APPLICATION NUMBER: 60/142,764
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 60/152,318
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 2881
;   LENGTH: 597
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(574)
;   OTHER INFORMATION: RXA02751
US-09-605-703B-2881

  Query Match             81.1%;  Score 15.4;  DB 4;  Length 597;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 AATGTCATCGTCCCCGG 18
              |||| ||||||||||||
Db        394 AATGCCATCGTCCCCGG 378


RESULT 11
US-09-949-016-136302
; Sequence 136302, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 136302
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-136302

  Query Match             81.1%;  Score 15.4;  DB 3;  Length 601;
  Best Local Similarity   94.1%;  Pred. No. 2.8e+02;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 ATGTCATCGTCCCCGGG 19
              ||||||| |||||||||
Db         61 ATGTCATTGTCCCCGGG 77


RESULT 12
US-09-582-337-1/c
; Sequence 1, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
;  APPLICANT: Japan Tobacco, Inc.
;  TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
;  TITLE OF INVENTION:  and Medicinal Uses Thereof
;  FILE REFERENCE: J1-009PCT
;  CURRENT APPLICATION NUMBER: US/09/582,337
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: JP P1997-367699
;  PRIOR FILING DATE: 1997-12-25
;  PRIOR APPLICATION NUMBER: JP P1998-356183
;  PRIOR FILING DATE: 1998-12-15
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2338
;   TYPE: DNA
;   ORGANISM: Rat
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(212)
;   NAME/KEY: CDS
;   LOCATION: (213)..(1256)
;   NAME/KEY: 3'UTR
;   LOCATION: (1257)..(2338)
;   NAME/KEY: polyA_signal
;   LOCATION: (2297)..(2302)
US-09-582-337-1
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Query Match 81.1%; Score 15.4; DB 3; Length 2338;
Best Local Similarity 94.1%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 ATGTCATCGTCCCCGGG 19
              ||||||| |||||||||
Db       1210 ATGTCATTGTCCCCGGG 1194
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RESULT 13
US-09-187-478-1/c
; Sequence 1, Application US/09187478
; Patent No. 6348329
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Brian F.
; APPLICANT: Allen, Margaret L.
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use
; FILE REFERENCE: 08766/004001
; CURRENT APPLICATION NUMBER: US/09/187,478
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-187-478-1

Query Match 81.1%; Score 15.4; DB 3; Length 2350;
Best Local Similarity 94.1%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 ATGTCATCGTCCCCGGG 19
              ||||||| |||||||||
Db       1209 ATGTCATTGTCCCCGGG 1193
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RESULT 14
US-09-292-036-1/c
; Sequence 1, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
; FILE REFERENCE: FIBRO1100-1
; CURRENT APPLICATION NUMBER: US/09/292,036
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (212)..(1252)
US-09-292-036-1

Query Match 81.1%; Score 15.4; DB 3; Length 2350;
Best Local Similarity 94.1%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 ATGTCATCGTCCCCGGG 19
              ||||||| |||||||||
Db       1209 ATGTCATTGTCCCCGGG 1193
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RESULT 15
US-09-949-016-15571/c
; Sequence 15571, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15571
; LENGTH: 51049
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15571

Query Match 81.1%; Score 15.4; DB 3; Length 51049;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 ATGTCATCGTCCCCGGG 19
              ||||||| |||||||||
Db      13225 ATGTCATTGTCCCCGGG 13209
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Search completed: December 2, 2005, 23:43:52
Job time : 6.25502 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 2, 2005, 23:40:24 ; Search time 254.827 Seconds
(without alignments)
1863.702 Million cell updates/sec

Title: US-09-979-558A-1
Perfect score: 1526
Sequence: 1 tttgatcatggctccagatt.....acctgcggctggatcacctc 1526

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	875.4	57.4	1513	7	US-11-055-637-79	Sequence 79, Appl
2	848.2	55.6	1548	6	US-10-793-568A-42	Sequence 42, Appl
3	847.6	55.5	1486	7	US-11-055-637-69	Sequence 69, Appl
4	845.4	55.4	1549	6	US-10-793-568A-40	Sequence 40, Appl
5	841.8	55.2	1548	6	US-10-793-568A-41	Sequence 41, Appl
6	840.4	55.1	1507	7	US-11-055-637-78	Sequence 78, Appl
7	839.2	55.0	1545	7	US-11-055-637-66	Sequence 66, Appl
8	822.2	53.9	1535	7	US-11-055-637-74	Sequence 74, Appl
9	822	53.9	1485	7	US-11-055-637-76	Sequence 76, Appl
c 10	821.2	53.8	3169	6	US-10-793-626-3356	Sequence 3356, Ap
11	821.2	53.8	3308	6	US-10-793-626-3905	Sequence 3905, Ap
c 12	819.6	53.7	3821	6	US-10-793-626-3967	Sequence 3967, Ap
c 13	818	53.6	3008	6	US-10-793-626-4460	Sequence 4460, Ap
c 14	818	53.6	3657	6	US-10-793-626-4187	Sequence 4187, Ap
15	817.2	53.6	1486	7	US-11-055-637-71	Sequence 71, Appl
16	815	53.4	1505	7	US-11-055-637-80	Sequence 80, Appl
17	806.8	52.9	1491	7	US-11-055-637-83	Sequence 83, Appl
18	799.8	52.4	1459	7	US-11-084-508-3	Sequence 3, Appli
19	797.2	52.2	1470	7	US-11-055-637-84	Sequence 84, Appl
20	796.8	52.2	1481	7	US-11-055-637-72	Sequence 72, Appl
21	791.2	51.8	1422	7	US-11-055-637-65	Sequence 65, Appl
22	788.8	51.7	3171	6	US-10-793-626-3537	Sequence 3537, Ap
c 23	784	51.4	3253	6	US-10-793-626-3955	Sequence 3955, Ap
24	777.2	50.9	1405	7	US-11-055-637-70	Sequence 70, Appl
25	768	50.3	1422	7	US-11-055-637-81	Sequence 81, Appl
26	761	49.9	1446	7	US-11-055-637-75	Sequence 75, Appl
27	759	49.7	1507	7	US-11-055-637-73	Sequence 73, Appl
28	758.4	49.7	1427	7	US-11-055-637-68	Sequence 68, Appl
29	754.4	49.4	1429	7	US-11-055-637-67	Sequence 67, Appl
30	753.4	49.4	1517	6	US-10-500-834-1	Sequence 1, Appli
31	748.4	49.0	1496	7	US-11-055-637-77	Sequence 77, Appl
32	706.6	46.3	1505	7	US-11-055-637-82	Sequence 82, Appl
33	700.4	45.9	1403	6	US-10-522-454-1	Sequence 1, Appli
c 34	668	43.8	3427	6	US-10-793-626-3884	Sequence 3884, Ap
c 35	569	37.3	2839	6	US-10-793-626-4362	Sequence 4362, Ap
c 36	558	36.6	1085	6	US-10-793-626-4463	Sequence 4463, Ap
37	545	35.7	4429	6	US-10-793-626-3664	Sequence 3664, Ap
38	542.2	35.5	2436	6	US-10-793-626-4424	Sequence 4424, Ap
39	517.4	33.9	3444	6	US-10-793-626-4356	Sequence 4356, Ap
c 40	503	33.0	3275	6	US-10-793-626-3557	Sequence 3557, Ap
c 41	449.4	29.4	3929	6	US-10-793-626-3610	Sequence 3610, Ap
42	447.8	29.3	3713	6	US-10-793-626-3378	Sequence 3378, Ap
c 43	420.6	27.6	2857	6	US-10-793-626-4004	Sequence 4004, Ap
44	324.8	21.3	3500	6	US-10-793-626-3882	Sequence 3882, Ap
45	324.8	21.3	3513	6	US-10-793-626-3351	Sequence 3351, Ap

ALIGNMENTS

RESULT 1
US-11-055-637-79
; Sequence 79, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 1513
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-79

Query Match 57.4%; Score 875.4; DB 7; Length 1513;
Best Local Similarity 76.5%; Pred. No. 2.8e-273;
Matches 1153; Conservative 0; Mismatches 339; Indels 16; Gaps 6;

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Qy          30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
               ||||||  || ||| ||||||||||||||| |     | | ||||||||| ||| |
Db           7 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAATGGATTAAGAGCTTGCTCTTATGAAGT 66

Qy          90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
               ||| || |   ||       |    | | || ||||| |  ||   |||||| ||| ||
Db          67 TAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTACCCATAAGACTGGGATAACTCCGG 126

Qy         150 GAAACTCGAATTAATACCGCAT----------ACGTCTACGGGAGAAAGCAGGGGNTCAT 199
               |||||  |  |||||||| ||          ||  |   |  ||||      |
Db         127 GAAACCGGGGCTAATACCGGATAATATTTTGAACTGCATAGTTCGAAATTGAAAGGCGGC 186

Qy         200 TAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCT 259
               |    ||  | ||  | ||||  ||   |||| |||||||| ||||| ||||| |||
Db         187 TTCGGCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTC 246
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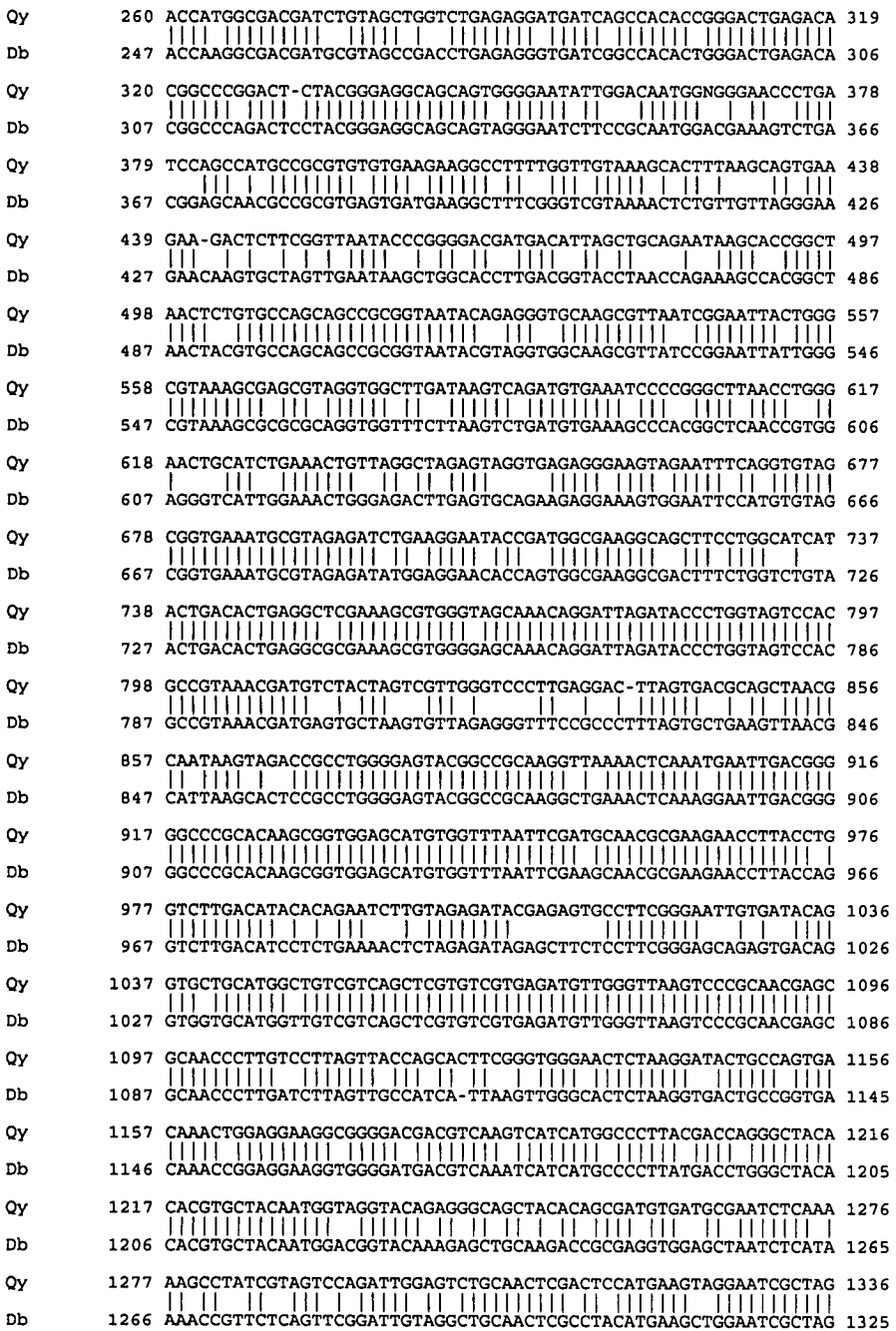

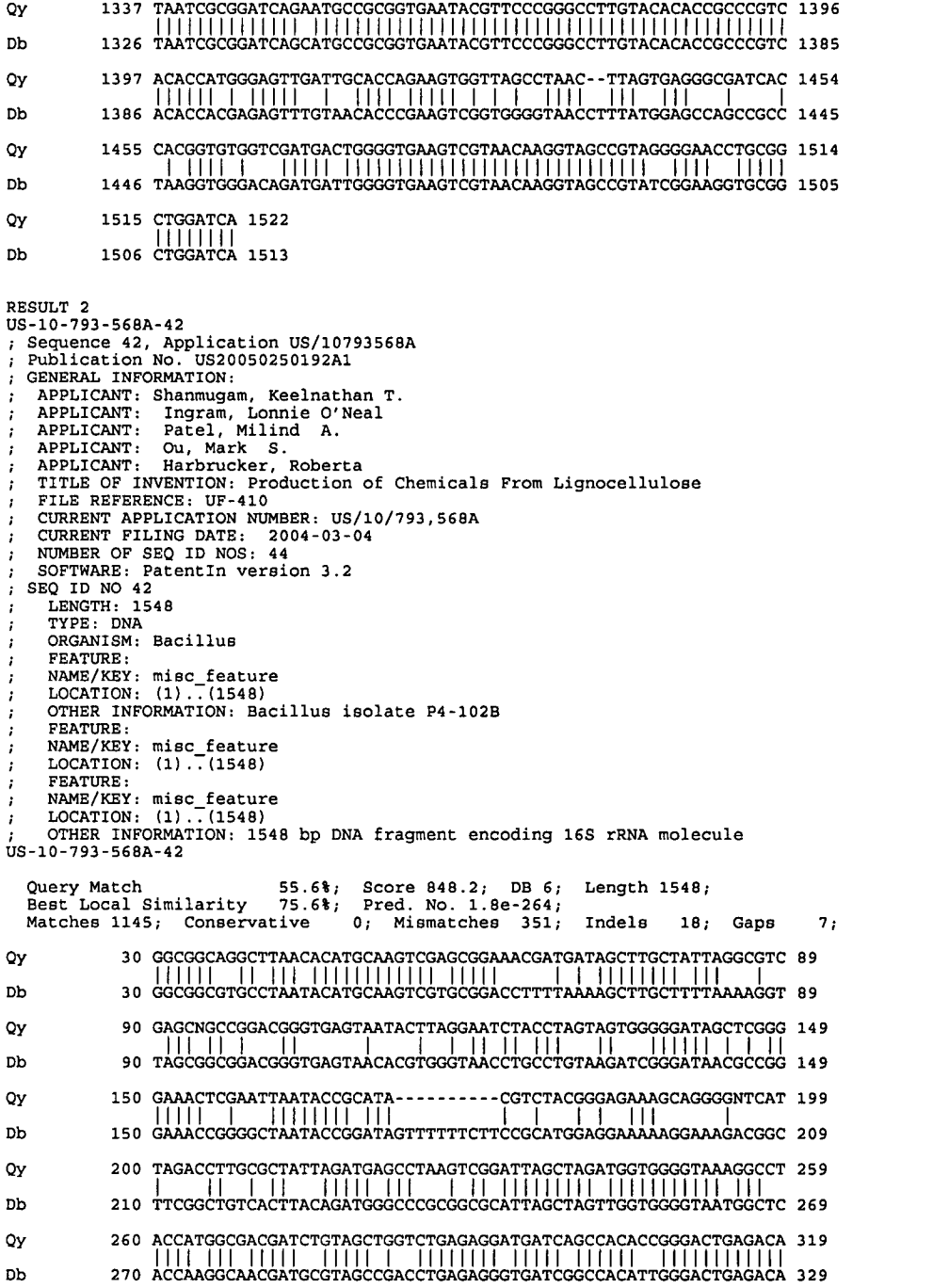

RESULT 2
US-10-793-568A-42
; Sequence 42, Application US/10793568A
; Publication No. US20050250192A1
; GENERAL INFORMATION:
; APPLICANT: Shanmugam, Keelnathan T.
; APPLICANT: Ingram, Lonnie O'Neal
; APPLICANT: Patel, Milind A.
; APPLICANT: Ou, Mark S.
; APPLICANT: Harbrucker, Roberta
; TITLE OF INVENTION: Production of Chemicals From Lignocellulose
; FILE REFERENCE: UF-410
; CURRENT APPLICATION NUMBER: US/10/793,568A
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Bacillus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1548)
; OTHER INFORMATION: Bacillus isolate P4-102B
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1548)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1548)
; OTHER INFORMATION: 1548 bp DNA fragment encoding 16S rRNA molecule
US-10-793-568A-42

Query Match 55.6%; Score 848.2; DB 6; Length 1548;
Best Local Similarity 75.6%; Pred. No. 1.8e-264;
Matches 1145; Conservative 0; Mismatches 351; Indels 18; Gaps 7;

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Qy       320 CGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGA 378
Db       330 CGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGA 389

Qy       379 TCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAA 438
Db       390 CGGAGCAACGCCGCGTGAGTGAAGAAGGCCTTCGGGTCGTAAAACTCTGTTGCCGGGGAA 449

Qy       439 GAAGACTCTTCGGT-TAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCT 497
Db       450 GAACAAGTGCCGTTCGAATAGGGCGGCGCCTTGACGGTACCCGGCCAGAAAGCCACGGCT 509

Qy       498 AACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGG 557
Db       510 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGG 569

Qy       558 CGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGG 617
Db       570 CGTAAAGCGCGCGCAGGCGGCTTCTTAAGTCTGATGTGAAATCTTGCGGCTCAACCGCAA 629

Qy       618 AACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAG 677
Db       630 GTGGTCATTGGAAACTGGGAGGCTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAG 689

Qy       678 CGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCAT 737
Db       690 CGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTA 749

Qy       738 ACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC 797
Db       750 ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 809

Qy       798 GCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAACG 856
Db       810 GCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCTAACG 869

Qy       857 CAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 916
Db       870 CATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGG 929

Qy       917 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 976
Db       930 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG 989

Qy       977 GTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATAC 1034
Db       990 GTCTTGACATCCTCTGACCTCCCTGGAGACAGGGCCTTCCCCTTCGGGGGACAGAGTGAC 1049

Qy      1035 AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1094
Db      1050 AGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1109

Qy      1095 GCGCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGT 1154
Db      1110 GCGCAACCCTTGACCTTAGTTGCCAGCA-TTCAGTTGGGCACTCTAAGGTGACTGCCGGT 1168

Qy      1155 GACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTA 1214
Db      1169 GACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA 1228

Qy      1215 CACACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCA 1274
Db      1229 CACACGTGCTACAATGGATGGTACAAAGGGCTGCGAGACCGCGAGGTTAAGCCAATCCCA 1288

Qy      1275 AAAAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCT 1334
Db      1289 GAAAACCATTCCCAGTTCGGATTGCAGGCTGCAACCCGCCTGCATGAAGCCGGAATCGCT 1348

Qy      1335 AGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1394
Db      1349 AGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1408

Qy      1395 TCACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAAC--TTAGTGAGGGCGATC 1452
Db      1409 TCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTACGGAGCCAGCCG 1468

Qy      1453 ACCACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGC 1512
Db      1469 CCGAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGC 1528

Qy      1513 GGCTGGATCACCTC 1526
Db      1529 GGCTGGATCACCTC 1542
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RESULT 3
US-11-055-637-69
; Sequence 69, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-69

Query Match 55.5%; Score 847.6; DB 7; Length 1486;
Best Local Similarity 76.1%; Pred. No. 2.8e-264;
Matches 1124; Conservative 0; Mismatches 337; Indels 16; Gaps 6;

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Qy        30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db        11 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAATGGATTAAGAGCTTGCTCTTATGAAGT 70

Qy        90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db        71 TAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAACTCCGG 130

Qy       150 GAAACTCGAATTAATACCGCAT----------ACGTCTACGGGAGAAAGCAGGGGNTCAT 199
Db       131 GAAACCGGGGCTAATACCGGATAACATTTTGAACCGCATGGTTCGAAATTGAAAGGCGGC 190

Qy       200 TAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCT 259
Db       191 TTCGGCTGTCACTTATGGATGGACCCGCGTCGCATTAGCTAGTTGGTGAGGTAACGGCTC 250

Qy       260 ACCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACA 319
Db       251 ACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACA 310

Qy       320 CGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGA 378
Db       311 CGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGA 370

Qy       379 TCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAA 438
Db       371 CGGAGCAACGCCGCGTGAGTGATGAAGGCTTTCGGGTCGTAAAACTCTGTTGTTAGGGAA 430

Qy       439 GAA-GACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCT 497
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                ||| | | | | |||| | || || |||| || ||    | |||| |||||
Db        431 GAACAAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCT 490

Qy        498 AACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGG 557
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Db        491 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGG 550

Qy        558 CGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGG 617
                ||||||||| ||| |||||| ||  |||||| |||||||| |||  |||| ||||  ||
Db        551 CGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGG 610

Qy        618 AACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAG 677
                |    |||  |||||||  || || ||||     ||||| |||| ||||| || ||||||
Db        611 AGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAG 670

Qy        678 CGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCAT 737
                |||||||||||||||||| || ||||| |||  ||||||||||  |||  ||||  |
Db        671 CGGTGAAATGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTA 730

Qy        738 ACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC 797
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Db        731 ACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 790

Qy        798 GCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAACG 856
                ||||||||||||  | |||  ||| |     ||  |  | ||||||  | || |||||
Db        791 GCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGAAGTTAACG 850

Qy        857 CAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 916
                || |||| |  ||||||||||||||||||||||||| | |||||||| ||||||||||
Db        851 CATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGG 910

Qy        917 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 976
                |||||||||||||||||||||||||||||||||||| ||||||||||||||||||| |
Db        911 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG 970

Qy        977 GTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAG 1036
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Db        971 GTCTTGACATCCTCTGAAAACCCTAGAGATAGGGCTTCTCCTTCGGGAGCAGAGTGACAG 1030

Qy       1037 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1096
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Db       1031 GTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1090

Qy       1097 GCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGA 1156
                |||||||||  |||||| ||| || ||  | |||| |||||||||  |||||| ||||
Db       1091 GCAACCCTTGATCTTAGTTGCCATCA-TTAAGTTGGGCACTCTAAGGTGACTGCCGGTGA 1149

Qy       1157 CAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1216
                ||||| |||||||| ||||| |||||||| |||||||| |||||| |||| ||||||||
Db       1150 CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACA 1209

Qy       1217 CACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAA 1276
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Db       1210 CACGTGCTACAATGGACGGTACAAAGAGCTGCAAGACCGCGAGGTGGAGCTAATCTCATA 1269

Qy       1277 AAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAG 1336
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Db       1270 AAACCGTTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGCTGGAATCGCTAG 1329

Qy       1337 TAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1396
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Db       1330 TAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1389

Qy       1397 ACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAACTTAGTGAGGGCGATC--AC 1454
                |||||| | ||||| |  |||| ||||| | | |  |||| |  |  | || | |   |
Db       1390 ACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGGGTAACCTTTTTGGAGCCAGCCGCC 1449

Qy       1455 CACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAA 1491
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Db       1450 TAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAA 1486


RESULT 4
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US-10-793-568A-40
; Sequence 40, Application US/10793568A
; Publication No. US20050250192A1
; GENERAL INFORMATION:
;  APPLICANT: Shanmugam, Keelnathan T.
;  APPLICANT:  Ingram, Lonnie O'Neal
;  APPLICANT:  Patel, Milind  A.
;  APPLICANT:  Ou, Mark  S.
;  APPLICANT:  Harbrucker, Roberta
;  TITLE OF INVENTION: Production of Chemicals From Lignocellulose
;  FILE REFERENCE: UF-410
;  CURRENT APPLICATION NUMBER: US/10/793,568A
;  CURRENT FILING DATE:  2004-03-04
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 1549
;   TYPE: DNA
;   ORGANISM: Bacillus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1549)
;   OTHER INFORMATION: 1549 bp DNA fragment encoding 16S rRNA molecule
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1549)
;   OTHER INFORMATION: Bacillus isolate 17C5
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (216)..(216)
;   OTHER INFORMATION: y = t or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (217)..(217)
;   OTHER INFORMATION: k = g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (254)..(254)
;   OTHER INFORMATION: w = a or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (268)..(268)
;   OTHER INFORMATION: y = t or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1461)..(1461)
;   OTHER INFORMATION: y = to or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1535)..(1535)
;   OTHER INFORMATION: y = t or c
US-10-793-568A-40

  Query Match             55.4%;  Score 845.4;  DB 6;  Length 1549;
  Best Local Similarity   75.4%;  Pred. No. 1.5e-263;
  Matches 1141;  Conservative    3;  Mismatches  352;  Indels   18;  Gaps    7;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              ||||||  || ||| |||||||||||| |||||      | | |||||||| |||   |
Db         34 GGCGGCGTGCCTAATACATGCAAGTCGTGCGGACCTTTTAAAAGCTTGCTTTTAAAAGGT 93

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
                ||| || |   ||       |    | | || || |||   ||   |||||| | | ||
Db         94 TAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGCCTGTAAGATCGGGATAACGCCGG 153

Qy        150 GAAACTCGAATTAATACCGCATA----------CGTCTACGGGAGAAAGCAGGGGNTCAT 199
              |||||  |   |||||||| |||          |   |  | |  |||       |
Db        154 GAAACCGGGGCTAATACCGGATAGTTTTTTCCTCCGCATGGAGGAAAAAGGAAAGACGGC 213

Qy        200 TAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCT 259
              |    ||  | ||   ||||| |||   | || |||||||:| ||||||||||| |||
Db        214 TTYKGCTGTCACTTACAGATGGGCCCGCGGCGCATTAGCTWGTTGGTGGGGTAAYGGCTC 273
```

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Qy       260 ACCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACA 319
Db       274 ACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACATTGGGACTGAGACA 333

Qy       320 CGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGA 378
Db       334 CGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGA 393

Qy       379 TCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAA 438
Db       394 CGGAGCAACGCCGCGTGAGTGAAGAAGGCCTTCGGGTCGTAAAACTCTGTTGCCGGGGAA 453

Qy       439 GAAGACTCTTCGGT-TAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCT 497
Db       454 GAACAAGTGCCGTTCGAACAGGGCGGCGCCTTGACGGTACCCGGCCAGAAAGCCACGGCT 513

Qy       498 AACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGG 557
Db       514 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGG 573

Qy       558 CGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGG 617
Db       574 CGTAAAGCGCGCGCAGGCGGCTTCTTAAGTCTGATGTGAAATCTTGCGGCTCAACCGCAA 633

Qy       618 AACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAG 677
Db       634 GCGGTCATTGGAAACTGGGAGGCTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAG 693

Qy       678 CGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCAT 737
Db       694 CGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTA 753

Qy       738 ACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC 797
Db       754 ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 813

Qy       798 GCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAACG 856
Db       814 GCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCTAACG 873

Qy       857 CAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 916
Db       874 CATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGG 933

Qy       917 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 976
Db       934 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG 993

Qy       977 GTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATAC 1034
Db       994 GTCTTGACATCCTCTGACCTCCCTGGAGACAGGGCCTTCCCCTTCGGGGGACAGAGTGAC 1053

Qy      1035 AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1094
Db      1054 AGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1113

Qy      1095 GCGCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGT 1154
Db      1114 GCGCAACCCTTGACCTTAGTTGCCAGCA-TTSAGTTGGGCACTCTAAGGTGACTGCCGGT 1172

Qy      1155 GACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTA 1214
Db      1173 GACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA 1232

Qy      1215 CACACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCA 1274
Db      1233 CACACGTGCTACAATGGATGGTACAAAGGGCTGCGAGACCGCGAGGTTAAGCCAATCCCA 1292

Qy      1275 AAAAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCT 1334
Db      1293 GAAAACCATTCCCAGTTCGGATTGCAGGCTGCAACCCGCCTGCATGAAGCCGGAATCGCT 1352

Qy      1335 AGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1394
Db      1353 AGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1412

Qy      1395 TCACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAAC--TTAGTGAGGGCGATC 1452
Db      1413 TCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTAYGGAGCCAGCCG 1472

Qy      1453 ACCACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGC 1512
Db      1473 CCGAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGC 1532

Qy      1513 GGCTGGATCACCTC 1526
Db      1533 GGYTGGATCACCTC 1546
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RESULT 5
US-10-793-568A-41
; Sequence 41, Application US/10793568A
; Publication No. US20050250192A1
; GENERAL INFORMATION:
; APPLICANT: Shanmugam, Keelnathan T.
; APPLICANT: Ingram, Lonnie O'Neal
; APPLICANT: Patel, Milind A.
; APPLICANT: Ou, Mark S.
; APPLICANT: Harbrucker, Roberta
; TITLE OF INVENTION: Production of Chemicals From Lignocellulose
; FILE REFERENCE: UF-410
; CURRENT APPLICATION NUMBER: US/10/793,568A
; CURRENT FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Bacillus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1548)
; OTHER INFORMATION: 1548 bp DNA fragment encoding 16S rRNA molecule
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1548)
; OTHER INFORMATION: Bacillus isolate 36D1
US-10-793-568A-41

Query Match 55.2%; Score 841.8; DB 6; Length 1548;
Best Local Similarity 75.4%; Pred. No. 2.1e-262;
Matches 1141; Conservative 0; Mismatches 355; Indels 18; Gaps 7;

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Qy        30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db        30 GGCGGCGTGCCTAATACATGCAAGTCGTGCGGACCTTTTAAAAGCTTGCTTTTAAAAGGT 89

Qy        90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db        90 TAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGATCGGGATAACGCCGG 149

Qy       150 GAAACTCGAATTAATACCGCATA----------CGTCTACGGGAGAAAGCAGGGGNTCAT 199
Db       150 GAAACCGGGGCTAATATCGGATAGTTTTTTCCTCCGCATGGAGGAAAAAGGAAAGACGGC 209

Qy       200 TAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCT 259
Db       210 TTTTGCTGTCACTTACAGATGGGCCCGCGGCGCATTAGCTAGTTGGTGGGGTAACGGCTC 269

Qy       260 ACCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACA 319
Db       270 ACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACATTGGGACTGAGACA 329

Qy       320 CGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGA 378
Db       330 CGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGA 389
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Qy        379 TCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAA 438
Db        390 CGGAGCAACGCCGCGTGAGTGAAGAAGGCCTTCGGGTCGTAAAACTCTGTTGCCGGGGAA 449

Qy        439 GAAGACTCTTCGGT-TAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCT 497
Db        450 GAACAAGTGCCGTTCGAACAGGGCGGCGCCTTGACGGTACCCGGCCAGAAAGCCACGGCT 509

Qy        498 AACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGG 557
Db        510 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGG 569

Qy        558 CGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGG 617
Db        570 CGTAAAGCGCGCGCAGGCGGTTTCTTAAGTCTGATGTGAAATCTTGCGGCTCAACCGCAA 629

Qy        618 AACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAG 677
Db        630 GCGGTCATTGGAAACTGGGGGGCTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGTAG 689

Qy        678 CGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCAT 737
Db        690 CGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTA 749

Qy        738 ACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC 797
Db        750 ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 809

Qy        798 GCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAACG 856
Db        810 GCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCTAACG 869

Qy        857 CAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 916
Db        870 CATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGG 929

Qy        917 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 976
Db        930 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG 989

Qy        977 GTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATAC 1034
Db        990 GTCTTGACATCCTCTGACCTCCCTGGAGACAGGGCCTTCCCCTTCGGGGGACAGAGTGAC 1049

Qy       1035 AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1094
Db       1050 AGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1109

Qy       1095 GCGCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGT 1154
Db       1110 GCGCAACCCTTGACCTTAGTTGCCAGCA-TTCAGTTGGGCACTCTAAGGTGACTGCCGGT 1168

Qy       1155 GACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTA 1214
Db       1169 GACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA 1228

Qy       1215 CACACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCA 1274
Db       1229 CACACGTGCTACAATGGATGGTACAAAGGGCTGCGAGACCGCGAGGTTAAGCCAATCCCA 1288

Qy       1275 AAAAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCT 1334
Db       1289 GAAAACCATTCCCAGTTCGGATTGCAGGCTGCAACCCGCCTGCATGAAGCCGGAATCGCT 1348

Qy       1335 AGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1394
Db       1349 AGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1408

Qy       1395 TCACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAAC--TTAGTGAGGGCGATC 1452
Db       1409 TCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTACGGAGCCAGCCG 1468

Qy       1453 ACCACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGC 1512
Db       1469 CCGAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGC 1528

Qy       1513 GGCTGGATCACCTC 1526
Db       1529 GGCTGGATCACCTC 1542
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RESULT 6
US-11-055-637-78
; Sequence 78, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 1507
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-78

Query Match 55.1%; Score 840.4; DB 7; Length 1507;
Best Local Similarity 77.1%; Pred. No. 6e-262;
Matches 1114; Conservative 0; Mismatches 313; Indels 17; Gaps 7;

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Qy         95 GCCGGACGGGTGAGTAATACTTAGG-AATCTACCTAGTAGTGGGGGATAGCTCGGGGAAA 153
Db         65 GGCGGACGGGTGAGTAACACGTGGGCAACCTGCCTATAAGACTGGGATAACTTCGGGAAA 124

Qy        154 CTCGAATTAATACCGCATACGTCTACGGGAGAAAGCAGGGGNTCATTAGA---------- 203
Db        125 CCGGAGCTAATACCGGATATGTTCTTCTCTCGCATGAGAGAAGATGGAAAGACGGTCTCG 184

Qy        204 CCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCA 263
Db        185 GCTGTCACTTATAGATGGGCCCGCGGCGCATTAGCTAGTTGGTGAGGTAATGGCTCACCA 244

Qy        264 TGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGC 323
Db        245 AGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC 304

Qy        324 CCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCA 382
Db        305 CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGA 364

Qy        383 GCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAG 442
Db        365 GCAACGCCGCGTGAACGATGAAGGCTTTCGGGTCGTAAAGTTCTGTTGTTAGGGAAGAAC 424

Qy        443 ACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTC 502
Db        425 AAGTACCAGAGTAACTGCTGGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTA 484

Qy        503 TGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAA 562
Db        485 CGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAA 544

Qy        563 AGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTG 622
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Db        545 AGCGCGCGCAGGTGGTTCCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGT 604

Qy        623 CATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTG 682

Db        605 CATTGGAAACTGGGGAACTTGAGTGTAGAAGAGGAAAGTGGAATTCCACGTGTAGCGGTG 664

Qy        683 AAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGA 742

Db        665 AAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTATAACTGA 724

Qy        743 CACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGT 802

Db        725 CACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGT 784

Qy        803 AAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAACGCAATA 861

Db        785 AAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCTAACGCATTA 844

Qy        862 AGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCC 921

Db        845 AGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGGCCC 904

Qy        922 GCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTT 981

Db        905 GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTT 964

Qy        982 GACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATACAGGTG 1039

Db        965 GACATCCTCTGACACTCCTAGAGATAGGACGTTCCCCTTCGGGGGACAGAGTGACAGGTG 1024

Qy       1040 CTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1099

Db       1025 GTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1084

Qy       1100 ACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAA 1159

Db       1085 ACCCTTGATCTTAGTTGCCAGCA-TTCAGTTGGGCACTCTAAGGTGACTGCCGGTGATAA 1143

Qy       1160 ACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACAC 1219

Db       1144 ACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACAC 1203

Qy       1220 GTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAG 1279

Db       1204 GTGCTACAATGGATGGTACAAAGAGCTGCAAACCCGCGAGGGTAAGCGAATCTCATAAAG 1263

Qy       1280 CCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAA 1339

Db       1264 CCATTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAA 1323

Qy       1340 TCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACA 1399

Db       1324 TCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACA 1383

Qy       1400 CCATGGGAGTTGATTGCACCAGAAGT-GGTTAGCCTAACTTAGTGAGGGCGATCACCACG 1458

Db       1384 CCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCGCAAGGAGCCAGCCGCCTAAG 1443

Qy       1459 GTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGG 1518

Db       1444 GTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGG 1503

Qy       1519 ATCA 1522

Db       1504 ATCA 1507


RESULT 7
US-11-055-637-66
; Sequence 66, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
;  APPLICANT: BROUSSEAU, Roland
;  APPLICANT:  DUBOIS, Jason
;  APPLICANT:  EDGE, Tom
;  APPLICANT:  MASSON, Luc
;  APPLICANT:  TREVORS, Jack T.
;  TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
;  TITLE OF INVENTION:  CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
;  FILE REFERENCE: 2139-33US
;  CURRENT APPLICATION NUMBER: US/11/055,637
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,288
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
;   LENGTH: 1545
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe for DNA array
US-11-055-637-66

  Query Match             55.0%;  Score 839.2;  DB 7;  Length 1545;
  Best Local Similarity   76.1%;  Pred. No. 1.5e-261;
  Matches 1152;  Conservative    0;  Mismatches  341;  Indels   20;  Gaps    9;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db         31 GGCGGCGTGCCTAATACATGCAAGTCGAGCGG-ACCGACGGGAGCTTGCTCCCTTAGGTC 89

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGG-AATCTACCTAGTAGTGGGGGATAGCTCGG 148

Db         90 --AGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCG 147

Qy        149 GGAAACTCGAATTAATACCGCATACGTCTACGGG-----------AGAAAGCAGGGGNTC 197

Db        148 GGAAACCGGGGCTAATACCGGATGCTTGATTGAACCGCATGGTTCAATCATAAAAGGTGG 207

Qy        198 ATTAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGC 257

Db        208 CTTTTAGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGC 267

Qy        258 CTACCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGA 317

Db        268 TCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGA 327

Qy        318 CACGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCT 376

Db        328 CACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCT 387

Qy        377 GATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTG 436

Db        388 GACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGGG 447

Qy        437 AAGAAGACTCTTCGGT-TAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGG 495

Db        448 AAGAACAAGTACCGTTCGAATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGCCACGG 507

Qy        496 CTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTG 555

Db        508 CTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTG 567

Qy        556 GGCGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTG 615

Db        568 GGCGTAAAGCGCGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGG 627

Qy        616 GGAACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGT 675

Db        628 GGAGGGTCATTGGAAACTGGGGAACTTGAGTGCAGAAGAGGAGAGTGGAATTCCACGTGT 687

Qy        676 AGCGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATC 735

Db        688 AGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTG 747
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Qy        736 ATACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCC 795
              |||||| ||||||| |||||||||||| ||| ||||||||||||||||||||||||||
Db        748 TAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCC 807

Qy        796 ACGCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAA 854
              |||||||||||||| | |||   ||| |     ||  |  | ||||||  ||||| ||
Db        808 ACGCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGCAAA 867

Qy        855 CGCAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACG 914
              |||| |||| |  |||||||||||||||| ||||||  | |||||||| |||||||||
Db        868 CGCATTAAGCACTCCGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACG 927

Qy        915 GGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACC 974
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        928 GGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACC 987

Qy        975 TGGTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATAC 1034
              |||||||||| | | ||      |||||||| |      ||||||||    | |  ||
Db        988 AGGTCTTGACATCCTCTGACAACCCTAGAGATAGGGCTTCCCCTTCGGGGGCAGAGTGAC 1047

Qy       1035 AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1094
              ||||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 AGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1107

Qy       1095 GCGCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGT 1154
              |||||||||||  ||||||| |||||| ||| | |||| |||||||||  |||||| ||
Db       1108 GCGCAACCCTTGATCTTAGTTGCCAGCA-TTCAGTTGGGCACTCTAAGGTGACTGCCGGT 1166

Qy       1155 GACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTA 1214
              ||||||| |||||||| ||||| |||||||| |||||||| ||||| |||| ||||||
Db       1167 GACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA 1226

Qy       1215 CACACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCA 1274
              ||||||||||||||||   | ||| |||||||| |  | |||| |  | || |||| ||
Db       1227 CACACGTGCTACAATGGGCAGAACAAAGGGCAGCGAAGCCGCGAGGCTAAGCCAATCCCA 1286

Qy       1275 AAAAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCT 1334
              ||| |   ||  ||| | ||| | |||||||||||||||| | |||||  |||||||||
Db       1287 CAAATCTGTTCTCAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGCTGGAATCGCT 1346

Qy       1335 AGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1394
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1347 AGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1406

Qy       1395 TCACACCATGGGAGTTGATTGCACCAGAAGT-GGTTAGCCTAACTTAGTGAGGGCGATCA 1453
              |||||||| | |||||  |  |||| ||||| ||| ||   | |||   |||   |
Db       1407 TCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTTGGAGCCAGCCGC 1466

Qy       1454 CCACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCG 1513
              | | |||| |   ||||| |||||||||||||||||||||||||||||  ||||  ||||
Db       1467 CGAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCG 1526

Qy       1514 GCTGGATCACCTC 1526
              |||||||||||||
Db       1527 GCTGGATCACCTC 1539


RESULT 8
US-11-055-637-74
; Sequence 74, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
;  APPLICANT: BROUSSEAU, Roland
;  APPLICANT:  DUBOIS, Jason
;  APPLICANT:  EDGE, Tom
;  APPLICANT:  MASSON, Luc
;  APPLICANT:  TREVORS, Jack T.
;  TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
;  TITLE OF INVENTION:  CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
;  FILE REFERENCE: 2139-33US
;  CURRENT APPLICATION NUMBER: US/11/055,637
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/543,288
;  PRIOR FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 1535
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe for DNA array
US-11-055-637-74

  Query Match             53.9%;  Score 822.2;  DB 7;  Length 1535;
  Best Local Similarity   76.6%;  Pred. No. 4.7e-256;
  Matches 1138;  Conservative    0;  Mismatches  326;  Indels   22;  Gaps   10;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              ||||||  || ||| |||||||||||||| |||  ||||  ||||||||   ||  ||
Db         31 GGCGGCGTGCCTAATACATGCAAGTCGAGC-GAATGGATGGGAGCTTGCTCCCAGAAGT- 88

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGG-AATCTACCTAGTAGTGGGGGATAGCTCGG 148
                 | ||||||||||||||| || | || || ||||||   ||   |||||| ||  |
Db         89 -TAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTACCTGTAAGACTGGGATAACTTCG 147

Qy        149 GGAAACTCGAATTAATACCGCATA--------CGTCTACGGGAGAAAGCAGGG--GNTCA 198
              ||||||  ||  |||||||| |||        | ||| | ||||||||    |    |
Db        148 GGAAACCGGAGCTAATACCGGATAACTTCTTTCTTCTCCTGGAGAAAGGTTGAAAGACGG 207

Qy        199 TTAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCC 258
              |    ||  | ||   ||||| |||   | || ||||||||| ||||| ||||| |||
Db        208 CTTCGGCTGTCACTTACAGATGGGCCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCT 267

Qy        259 TACCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGAC 318
              |||| ||| |||||  |||| |  |||||||| |||||  |||||| ||||||||||||
Db        268 CACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGAC 327

Qy        319 ACGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGNGGGAACCCTG 377
              ||||||| |||| |||||||||||||||| |||||| ||   ||||||  | ||  |||
Db        328 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTG 387

Qy        378 ATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGA 437
              |   ||| | |||||||| |||| |||||  ||  | | ||||| | || | | ||| ||
Db        388 ACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAACTCTGTTATCAGGGA 447

Qy        438 AGAAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCT 497
              |||| |    ||||     | || ||  |||| || |||   |  ||||  |||||
Db        448 AGAACAAGTATCGGAGTAACTGCCGGTACCTTGACGGTACCTGACCAGAAAGCCACGGCT 507

Qy        498 AACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGG 557
              ||||  |||||||||||||||||||||  |||  |||||||||   |||||||| ||||
Db        508 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGG 567

Qy        558 CGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGG 617
              ||||||||| ||| ||| || ||  |||||| |||||||| |||  |||| ||||  ||
Db        568 CGTAAAGCGCGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGG 627

Qy        618 AACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAG 677
              ||   |||  |||||||  || || ||||      ||||   ||  ||||| || ||||||
Db        628 AAGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAGAGAAGAGCGGAATTCCACGTGTAG 687

Qy        678 CGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCAT 737
              |||||||||||||||||| || ||||| |||  |||||||||| |||   |||  |
Db        688 CGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCTCTTTGGTCTGTA 747

Qy        738 ACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC 797
              |||||| ||||||| |||||||||||| ||| ||||||||||||||||||||||||||||
Db        748 ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCAC 807

Qy        798 GCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGAC-TTAGTGACGCAGCTAACG 856
              |||||||||||||  | |||   ||| |     ||  |  | ||||||  |||| |||||
Db        808 GCCGTAAACGATGAGTGCTAAGTGTTAGAGGGTTTCCGCCCTTTAGTGCTGCAGTTAACG 867

Qy        857 CAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 916
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Db        868 CATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGG 927

Qy        917 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 976

Db        928 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG 987

Qy        977 GTCTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATAC 1034

Db        988 GTCTTGACATCCTCTGACCACCCTAGAGATAGGGACTTCCCCTTCGGGGGACAGAGTGAC 1047

Qy       1035 AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1094

Db       1048 AGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1107

Qy       1095 GCGCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGT 1154

Db       1108 GCGCAACCCTTAACCTTAGTTGCCAGCA-TTCAGTTGGGCACTCTAAGGTGACTGCCGGT 1166

Qy       1155 GACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTA 1214

Db       1167 GACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA 1226

Qy       1215 CACACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCA 1274

Db       1227 CACACGTGCTACAATGGATGGTACAAAGGGTTGCAAGACCGCGAGGTTTAGCTAATCCCA 1286

Qy       1275 AAAAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCT 1334

Db       1287 TAAAACCATTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCT 1346

Qy       1335 AGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1394

Db       1347 AGTAATCGTGGATCAGCATGCCACGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1406

Qy       1395 TCACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAAC---TTAGTGAGGGCGAT 1451

Db       1407 TCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGGGTAACCCTTACGGGAGCCAGCC 1466

Qy       1452 CACCACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGC 1497

Db       1467 GCCGAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAAGGTAGC 1512
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RESULT 9
US-11-055-637-76
; Sequence 76, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-76

Query Match 53.9%; Score 822; DB 7; Length 1485;
Best Local Similarity 76.7%; Pred. No. 5.3e-256;

Matches 1135; Conservative 0; Mismatches 323; Indels 21; Gaps 10;

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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db         11 GGCGGCATGCCTAATACATGCAAGTCGAGCGG-AATGACGAGAGCTTGCTCTCTG--ATT 67

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGG-AATCTACCTAGTAGTGGGGGATAGCTCGG 148

Db         68 TTAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGCCCTACAGATGGGGATAACTCCG 127

Qy        149 GGAAACTCGAATTAATACCGCATA----------CGTCTACGGGAGAAAGCAGGGGNTCA 198

Db        128 GGAAACCGGGGCTAATACCGAATAATCAGTTTGTCCGCATGGACAAACTCTGAAAGACGG 187

Qy        199 TTAGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCC 258

Db        188 TTTCGGCTGTCACTGTAGGATGGGCCCGCGGCGCATTAGCTAGTTGGTGGGGTAATGGCC 247

Qy        259 TACCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGAC 318

Db        248 TACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGAC 307

Qy        319 ACGGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTG 377

Db        308 ACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCACAATGGACGAAAGTCTG 367

Qy        378 ATCCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGA 437

Db        368 ATGGAGCAATGCCGCGTGAGCGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGGGA 427

Qy        438 AGAAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCT 497

Db        428 AGAACACGTACGGGAGTAACTGCCCGTGCCATGACGGTACCTTATTAGAAAGCCACGGCT 487

Qy        498 AACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGG 557

Db        488 AACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGG 547

Qy        558 CGTAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGG 617

Db        548 CGTAAAGCGCGCGCAGGCGGTTCTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGG 607

Qy        618 AACTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAG 677

Db        608 AGGGTCATTGGAAACTGGAGAACTTGAGTACAGAAGAGGAAAGCGGAATTCCACGTGTAG 667

Qy        678 CGGTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCAT 737

Db        668 CGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGGCTTTCTGGTCTGTA 727

Qy        738 ACTGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCAC 797

Db        728 ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCAC 787

Qy        798 GCCGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAG-GACTTAGTGACGCAGCTAACG 856

Db        788 GCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACG 847

Qy        857 CAATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGG 916

Db        848 CATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGG 907

Qy        917 GGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTG 976

Db        908 GACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAG 967

Qy        977 GTCTTGACAT-ACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGAT-AC 1034

Db        968 GTCTTGACATCCCACTGACCGGTGTAGAGATACGCCTTTCCCTTCGGGGACAGTGGTGAC 1027

Qy       1035 AGGTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1094

Db       1028 AGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGA 1087
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Qy       1095 GCGCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGT 1154
Db       1088 GCGCAACCCTTGATCTTAGTTGCCAGCA-TTCAGTTGGGCACTCTAAGGTGACTGCCGGT 1146

Qy       1155 GACAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTA 1214
Db       1147 GATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTA 1206

Qy       1215 CACACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCA 1274
Db       1207 CACACGTGCTACAATGGATGATACAGAGGGTTGCCAACCCGCGAGGGGGAGCCAATCCCA 1266

Qy       1275 AAAAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCT 1334
Db       1267 TAAAATCGTTCCCAGTTCGGATTGGAGGCTGCAACTCGCCTCCATGAAGTTGGAATCGCT 1326

Qy       1335 AGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCG 1394
Db       1327 AGTAATCGTGGATCAGCATGCCACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCG 1386

Qy       1395 TCACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCT--AACTTAGTGAGGGCGATC 1452
Db       1387 TCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGGGGTACATCTACGGGAGCCAGCCG 1446

Qy       1453 ACCACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAA 1491
Db       1447 CCGAAGGTGGGACAGATGATTGGGGTGAAGTCGTAACAA 1485


RESULT 10
US-10-793-626-3356/c
; Sequence 3356, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3356
;   LENGTH: 3169
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3356

  Query Match             53.8%;  Score 821.2;  DB 6;  Length 3169;
  Best Local Similarity   74.1%;  Pred. No. 1.4e-255;
  Matches 1120;  Conservative    0;  Mismatches  376;  Indels   15;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db       2809 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGACGAGGAGCTTGCTCCTCTGACGT 2750

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db       2749 TAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGG 2690

Qy        150 GAAACTCGAATTAATACCGCAT---------ACGTCTACGGGAGAAAGCAGGGGNTCATT 200
Db       2689 GAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAATAGTGAAAGACGGT 2630

Qy        201 AGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTA 260
Db       2629 TTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAACGGCTTA 2570

Qy        261 CCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACAC 320
Db       2569 CCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACAC 2510

Qy        321 GGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGAT 379
Db       2509 GGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGAC 2450

Qy        380 CCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAG 439
Db       2449 GGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAG 2390

Qy        440 AAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAA 499
Db       2389 AACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAA 2330

Qy        500 CTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCG 559
Db       2329 CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCG 2270

Qy        560 TAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAA 619
Db       2269 TAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAG 2210

Qy        620 CTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCG 679
Db       2209 GGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCG 2150

Qy        680 GTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATAC 739
Db       2149 GTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAAC 2090

Qy        740 TGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGC 799
Db       2089 TGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGC 2030

Qy        800 CGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGA-CTTAGTGACGCAGCTAACGCA 858
Db       2029 CGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCA 1970

Qy        859 ATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG 918
Db       1969 TTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGA 1910

Qy        919 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGT 978
Db       1909 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAAT 1850

Qy        979 CTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATACAG 1036
Db       1849 CTTGACATCCTCTGACCCCTCTAGAGATAGAGTTTTCCCCTTCGGGGGACAGAGTAACAG 1790

Qy       1037 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1096
Db       1789 GTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1730

Qy       1097 GCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGA 1156
Db       1729 GCAACCCTTAAGCTTAGTTGCCATCA-TTAAGTTGGGCACTCTAAGTTGACTGCCGGTGA 1671

Qy       1157 CAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1216
Db       1670 CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACA 1611

Qy       1217 CACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAA 1276
Db       1610 CACGTGCTACAATGGACAATACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATA 1551

Qy       1277 AAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAG 1336
Db       1550 AAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTATATGAAGCTGGAATCGCTAG 1491

Qy       1337 TAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1396
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Db       1490 TAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 1431

Qy       1397 ACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACC 1455

Db       1430 ACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCATTTGGAGCTAGCCGTCG 1371

Qy       1456 ACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGC 1515

Db       1370 AAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGC 1311

Qy       1516 TGGATCACCTC 1526

Db       1310 TGGATCACCTC 1300


RESULT 11
US-10-793-626-3905
; Sequence 3905, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3905
;   LENGTH: 3308
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3905

  Query Match             53.8%;  Score 821.2;  DB 6;  Length 3308;
  Best Local Similarity   74.1%;  Pred. No. 1.4e-255;
  Matches 1120;  Conservative    0;  Mismatches  376;  Indels   15;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db        243 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGACGAGGAGCTTGCTCCTCTGACGT 302

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db        303 TAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGG 362

Qy        150 GAAACTCGAATTAATACCGCAT---------ACGTCTACGGGAGAAAGCAGGGGNTCATT 200

Db        363 GAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAATAGTGAAAGACGGT 422

Qy        201 AGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTA 260

Db        423 TTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAACGGCTTA 482

Qy        261 CCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACAC 320

Db        483 CCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACAC 542

Qy        321 GGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGAT 379

Db        543 GGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGAC 602

Qy        380 CCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAG 439

Db        603 GGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAG 662

Qy        440 AAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAA 499

Db        663 AACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAA 722

Qy        500 CTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCG 559

Db        723 CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCG 782

Qy        560 TAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAA 619

Db        783 TAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAG 842

Qy        620 CTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCG 679

Db        843 GGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCG 902

Qy        680 GTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATAC 739

Db        903 GTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAAC 962

Qy        740 TGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGC 799

Db        963 TGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGC 1022

Qy        800 CGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGA-CTTAGTGACGCAGCTAACGCA 858

Db       1023 CGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCA 1082

Qy        859 ATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG 918

Db       1083 TTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGA 1142

Qy        919 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGT 978

Db       1143 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAAT 1202

Qy        979 CTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATACAG 1036

Db       1203 CTTGACATCCTCTGACCCCTCTAGAGATAGAGTTTCCCCTTCGGGGGACAGAGTAACAG 1262

Qy       1037 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1096

Db       1263 GTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1322

Qy       1097 GCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGA 1156

Db       1323 GCAACCCTTAAGCTTAGTTGCCATCA-TTAAGTTGGGCACTCTAAGTTGACTGCCGGTGA 1381

Qy       1157 CAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1216

Db       1382 CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACA 1441

Qy       1217 CACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAA 1276

Db       1442 CACGTGCTACAATGGACAATACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATA 1501

Qy       1277 AAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAG 1336

Db       1502 AAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTATATGAAGCTGGAATCGCTAG 1561

Qy       1337 TAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1396

Db       1562 TAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 1621

Qy       1397 ACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACC 1455

Db       1622 ACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCATTTGGAGCTAGCCGTCG 1681

Qy       1456 ACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGC 1515

Db       1682 AAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGC 1741

Qy       1516 TGGATCACCTC 1526

Db       1742 TGGATCACCTC 1752
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```
RESULT 12
US-10-793-626-3967/c
; Sequence 3967, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3967
;   LENGTH: 3821
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3967

  Query Match             53.7%;  Score 819.6;  DB 6;  Length 3821;
  Best Local Similarity   74.1%;  Pred. No. 5e-255;
  Matches 1119;  Conservative    0;  Mismatches  377;  Indels   15;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              ||||||  || ||| ||||||||||||||| | |       |||||||  |  |
Db       3616 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGACGAGGAGCTTGCTCCTCTGACGT 3557

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              ||| || |   ||      |     || |||||||  ||   ||||||  ||  ||
Db       3556 TAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGG 3497

Qy        150 GAAACTCGAATTAATACCGCAT---------ACGTCTACGGGAGAAAGCAGGGGNTCATT 200
              |||||  ||  |||||||| ||         |  ||   ||     |    | |
Db       3496 GAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAATAGTGAAAGACGGT 3437

Qy        201 AGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTA 260
                 ||  | ||  ||||||    |    | || |||||||| ||||  ||||| ||| ||
Db       3436 TTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAACGGCTTA 3377

Qy        261 CCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACAC 320
              ||| ||| |||||  ||||| |  ||||||| ||||| |||||||  || ||||||||||
Db       3376 CCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACAC 3317

Qy        321 GGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGAT 379
              || || |||| |||||||||||||||||| |||||| ||    ||||||  | || |||||
Db       3316 GGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGAC 3257

Qy        380 CCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAG 439
                 ||| | ||||||||  |||| ||||| |||  | | |||||  | || | |   || ||||
Db       3256 GGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAG 3197

Qy        440 AAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAA 499
              || |    |     |     |      ||||  || ||    |  ||||  |||||||
Db       3196 AACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAA 3137

Qy        500 CTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCG 559
              ||  |||||||||||||||||||||   |||  ||||||||||  |||||||| ||||||
Db       3136 CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCG 3077

Qy        560 TAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAA 619
              |||||||  |||||||  || ||  ||||||  |||||||| |||  ||||  ||||   |||
Db       3076 TAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAG 3017

Qy        620 CTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCG 679
                 |||  |||||||   |  ||  ||||     |||||  ||||  |||||  || ||||||||
Db       3016 GGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCG 2957

Qy        680 GTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATAC 739
              |||||||||| ||||||  || |||||  |||  ||||||||||  |||  ||||  |    ||
Db       2956 GTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAAC 2897

Qy        740 TGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGC 799
              ||||  |||| |  |||||||||||| | |||||||||||||||||||||||||||||||
Db       2896 TGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGC 2837

Qy        800 CGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGA-CTTAGTGACGCAGCTAACGCA 858
              ||||||||||  | |||   ||| ||    ||   |   |||||||  ||||||||||
Db       2836 CGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCA 2777

Qy        859 ATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG 918
              ||||  |  |||||||||||||||| |||||||||  |||||||| ||||||||||
Db       2776 TTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGA 2717

Qy        919 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGT 978
              |||||||||||||||||||||||||||||||| ||||||||||||||||||    |
Db       2716 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAAT 2657

Qy        979 CTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATACAG 1036
              |||||||| | | ||  | | |||||||       | ||  |  ||| |  | |  ||||
Db       2656 CTTGACATCCTCTGACCCCTCTAGAGATAGAGTTTTCCCCTTCGGGGGACAGAGTGACAG 2597

Qy        1037 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1096
               ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2596 GTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 2537

Qy        1097 GCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGA 1156
               |||||||||    ||||||| ||| || ||  | |||| ||||||||   ||||||  ||||
Db       2536 GCAACCCTTAAGCTTAGTTGCCATCA-TTAAGTTGGGCACTCTAAGTTGACTGCCGGTGA 2478

Qy        1157 CAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1216
               ||||| |||||||||  ||||| ||||||||  |||||||| ||||||  ||   ||||||||
Db       2477 CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACA 2418

Qy        1217 CACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAA 1276
               |||||||||||||||    |||| ||||||||  | ||  |||| ||  | ||  |||| || |
Db       2417 CACGTGCTACAATGGACAATACAAAGGGCAGCGAAACTGCGAGGTCAAGCAAATCCCATA 2358

Qy        1277 AAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAG 1336
               |||     ||  ||| | |||||  |||||||||||||||   ||||||  ||||||||||
Db       2357 AAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTATATGAAGCTGGAATCGCTAG 2298

Qy        1337 TAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1396
               ||||||  |||||| ||||  |||||||||||||||||| |||||||||||||||||||
Db       2297 TAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 2238

Qy        1397 ACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACC 1455
               ||||||  | |||||  |  |||| ||||  |  |  |||  | |   |||  |    |
Db       2237 ACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCATTTGGAGCTAGCCGTCG 2178

Qy        1456 ACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGC 1515
               | |||| |    |||| ||||||||||||||||||||||||||||  ||||  ||||||
Db       2177 AAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGC 2118

Qy        1516 TGGATCACCTC 1526
               ||||||||||
Db       2117 TGGATCACCTC 2107


RESULT 13
US-10-793-626-4460/c
; Sequence 4460, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
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;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4460
;   LENGTH: 3008
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4460

  Query Match            53.6%;  Score 818;  DB 6;  Length 3008;
  Best Local Similarity  74.0%;  Pred. No. 1.5e-254;
  Matches 1118;  Conservative    0;  Mismatches  378;  Indels   15;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||| || ||| |||||||||||||||| | |       |||||||| | |
Db       1517 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGACGAGGAGCTTGCTCCTCTGACGT 1458

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              ||| || |   ||      |    |   || |||||||  ||  |||||| ||  ||
Db       1457 TAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGG 1398

Qy        150 GAAACTCGAATTAATACCGCAT---------ACGTCTACGGGAGAAAGCAGGGGNTCATT 200
              |||||  ||  |||||||| ||         |    | ||   ||     |   | |
Db       1397 GAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAATAGTGAAAGACGGT 1338

Qy        201 AGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTA 260
                 ||  | ||  ||||||    |    | || |||||||| ||||  ||||| ||| ||
Db       1337 TTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAACGGCTTA 1278

Qy        261 CCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACAC 320
              ||| ||| |||||  |||||  |  |||||||| ||||| ||||||| || ||||||||||
Db       1277 CCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACAC 1218

Qy        321 GGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGAT 379
              || || |||| |||||||||||||||||| |||||| ||    ||||||   | || | |||
Db       1217 GGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCTTGAC 1158

Qy        380 CCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAG 439
                 ||| | |||||||| |||| ||||| |||  | | |||| | || | |  || ||||
Db       1157 GGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAG 1098

Qy        440 AAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAA 499
              || |     |      |      |    |||| || ||     |  ||||  |||||||
Db       1097 AACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAA 1038

Qy        500 CTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCG 559
              ||  |||||||||||||||||||||  |||  |||||||||  |||||||| ||||||
Db       1037 CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCG 978

Qy        560 TAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAA 619
              ||||||| ||||||| || ||  |||||| |||||||| |||  |||| ||||  |||
Db        977 TAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAG 918

Qy        620 CTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCG 679
                 |||  |||||||  |  || ||||     ||||| |||| ||||| || ||||||||
Db        917 GGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCG 858

Qy        680 GTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATAC 739
              |||||||||| |||||| || ||||| |||  ||||||||||  ||| ||||  |    ||
Db        857 GTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAAC 798

Qy        740 TGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGC 799
              |||| |||| |  |||||||||||| | ||||||||||||||||||||||||||||||
Db        797 TGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGC 738

Qy        800 CGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGA-CTTAGTGACGCAGCTAACGCA 858
              |||||||||| | |||   ||| ||    || |   |||||||  ||||||||||||
Db        737 CGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCA 678

Qy        859 ATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG 918
              |||| |  |||||||||||||||| |||||||||| |||||||||  ||||||||||||

Db        677 TTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGA 618

Qy        919 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGT 978
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||  |
Db        617 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAAT 558

Qy        979 CTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATACAG 1036
              ||||||| | | ||  | | |||||||    |  | ||  |  ||| |  |    ||||
Db        557 CTTGACATCCTCTGATCCCTCTAGAGATAGAGGTTTCCCCTTCGGGGGACAGAATGACAG 498

Qy       1037 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1096
              ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 GTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 438

Qy       1097 GCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGA 1156
              |||||||||   ||||||| ||| || ||  | |||| ||||||||   |||||| ||||
Db        437 GCAACCCTTAAGCTTAGTTGCCATCA-TTAAGTTGGGCACTCTAAGTTGACTGCCGGTGA 379

Qy       1157 CAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1216
              |||||  |||||||||  |||||  |||||||| |||||||| |||||  ||   ||||||||
Db        378 CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACA 319

Qy       1217 CACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAA 1276
              ||||||||||||||     |||| |||||||| | || |||| || | || |||| || |
Db        318 CACGTGCTACAATGGACAATACAAAGGGCAGCGAAACCGCGAGGTCAAGCAAATCCCATA 259

Qy       1277 AAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAG 1336
              |||    ||  ||| | ||||| |||||||||||||||  ||||||  ||||||||||
Db        258 AAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTATATGAAGCTGGAATCGCTAG 199

Qy       1337 TAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1396
              ||||||  |||||| |||  |||||||||||||||||||| ||||||||||||||||||||
Db        198 TAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 139

Qy       1397 ACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACC 1455
              |||||| | |||||  |  |||| |||| | | |  ||| | |  |||  |    |
Db        138 ACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCATTTGGAGCTAGCCGTCG 79

Qy       1456 ACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGC 1515
              | |||| |    |||| |||||||||||||||||||||||||||  |||| ||||||
Db          78 AAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGC 19

Qy       1516 TGGATCACCTC 1526
              ||||||||||
Db          18 TGGATCACCTC 8


RESULT 14
US-10-793-626-4187/c
; Sequence 4187, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4187
;   LENGTH: 3657
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4187

  Query Match            53.6%;  Score 818;  DB 6;  Length 3657;
  Best Local Similarity  74.0%;  Pred. No. 1.6e-254;
  Matches 1118;  Conservative    0;  Mismatches  378;  Indels   15;  Gaps    6;
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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              ||||||  || ||| |||||||||||||||| | |       ||||||||  |  |
Db       1617 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAACAGACGAGGAGCTTGCTCCTCTGACGT 1558

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              ||| || |   ||    |   |   || |||||||  ||   |||||| ||  ||
Db       1557 TAGCGGCGGACGGGTGAGTAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGG 1498

Qy        150 GAAACTCGAATTAATACCGCAT---------ACGTCTACGGGAGAAAGCAGGGGNTCATT 200
              |||||  ||  ||||||||  ||        |    | ||   ||    |      |  |
Db       1497 GAAACCGGAGCTAATACCGGATAATATATTGAACCGCATGGTTCAATAGTGAAAGACGGT 1438

Qy        201 AGACCTTGCGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTA 260
              ||  | ||  ||||||   |   | || |||||||| ||||  |||||  ||| ||
Db       1437 TTTGCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAACGGCTTA 1378

Qy        261 CCATGGCGACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACAC 320
              ||| ||| |||||  ||||| |  |||||||| |||||  ||||||| || ||||||||||
Db       1377 CCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACAC 1318

Qy        321 GGCCCGGACT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGAT 379
              || || |||| |||||||||||||||||| ||||||  ||    ||||||  |  || |||||
Db       1317 GGTCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGAC 1258

Qy        380 CCAGCCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAG 439
              |||  | ||||||||  |||| |||||  |||   |  | |||||  | ||  |  ||  ||||
Db       1257 GGAGCAACGCCGCGTGAGTGATGAAGGTCTTCGGATCGTAAAACTCTGTTATTAGGGAAG 1198

Qy        440 AAGACTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAA 499
              || |   |     |     |      ||||  ||  ||     |  ||||  |||||||
Db       1197 AACAAATGTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGGCTAA 1138

Qy        500 CTCTGTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCG 559
              ||  |||||||||||||||||||||  |||  ||||||||||  |||||||| ||||||
Db       1137 CTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCG 1078

Qy        560 TAAAGCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAA 619
              |||||||  |||||||  ||  ||  ||||||  |||||||||  |||   ||||  ||||  |||
Db       1077 TAAAGCGCGCGTAGGCGGTTTTTTAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAG 1018

Qy        620 CTGCATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCG 679
                 |||  |||||||  |   ||  ||||      |||||  ||||  |||||  ||  ||||||||
Db       1017 GGTCATTGGAAACTGGAAAACTTGAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCG 958

Qy        680 GTGAAATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATAC 739
              ||||||||||  ||||||  ||  |||||  |||   ||||||||||  |||  ||||   ||
Db       957 GTGAAATGCGCAGAGATATGGAGGAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAAC 898

Qy        740 TGACACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGC 799
              ||||  ||||  |   |||||||||||| | ||||||||||||||||||||||||||||||
Db       897 TGACGCTGATGTGCGAAAGCGTGGGGATCAAACAGGATTAGATACCCTGGTAGTCCACGC 838

Qy        800 CGTAAACGATGTCTACTAGTCGTTGGGTCCCTTGAGGA-CTTAGTGACGCAGCTAACGCA 858
              ||||||||||  | |||   ||| ||     ||  |   |||||||  ||||||||||||
Db       837 CGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCA 778

Qy        859 ATAAGTAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGG 918
              ||||  |  ||||||||||||||||| ||||||||| |||||||| ||||||||||||
Db       777 TTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGA 718

Qy        919 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGT 978
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||    |
Db       717 CCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAAT 658

Qy        979 CTTGACATACACAGAATCTTGTAGAGATACGAGAGTGCC--TTCGGGAATTGTGATACAG 1036
              ||||||||  | |  ||  | | ||||||||     |  ||   |  |||  | |  ||||
Db       657 CTTGACATCCTCTGACCCCTCTAGAGATAGAGTTTTCCCCTTCGGGGGACAGAGTGACAG 598

Qy       1037 GTGCTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 1096
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 GTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGC 538

Qy       1097 GCAACCCTTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGA 1156
              |||||||||   |||||| ||| || ||  | |||| ||||||||   |||||| ||||
Db        537 GCAACCCTTAAGCTTAGTTGCCATCA-TTAAGTTGGGCACTCTAAGTTGACTGCCGGTGA 479

Qy       1157 CAAACTGGAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACA 1216
              ||||| ||||||||| |||| |||||||| |||||||| |||||| ||   ||||||||
Db        478 CAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACA 419

Qy       1217 CACGTGCTACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAA 1276
              ||||||||||||||    |||| |||| ||| | || |||| || | || |||| || |
Db        418 CACGTGCTACAATGGACAATACAAAGGGTAGCGAAACCGCGAGGTCAAGCAAATCCCATA 359

Qy       1277 AAGCCTATCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAG 1336
              |||     ||  ||| | ||||| |||||||||||||||  ||||||  ||||||||||
Db        358 AAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTATATGAAGCTGGAATCGCTAG 299

Qy       1337 TAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTC 1396
              ||||||  |||||| |||| |||||||||||||||||| ||||||||||||||||||||
Db        298 TAATCGTAGATCAGCATGCTACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTC 239

Qy       1397 ACACCATGGGAGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACC 1455
              |||||| | |||||  |  |||| |||  | | |  ||| | |  |||  |   |  |
Db        238 ACACCACGAGAGTTTGTAACACCCGAAGCCGGTGGAGTAACCATTTGGAGCTAGCCGTCG 179

Qy       1456 ACGGTGTGGTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGC 1515
              | |||| |    |||| ||||||||||||||||||||||||||||||  ||||  ||||||
Db        178 AAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGC 119

Qy       1516 TGGATCACCTC 1526
              ||||||||||
Db        118 TGGATCACCTC 108
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RESULT 15
US-11-055-637-71
; Sequence 71, Application US/11055637
; Publication No. US20050260619A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: DUBOIS, Jason
; APPLICANT: EDGE, Tom
; APPLICANT: MASSON, Luc
; APPLICANT: TREVORS, Jack T.
; TITLE OF INVENTION: A DNA MICROARRAY FOR FINGERPRINTING AND
; TITLE OF INVENTION: CHARACTERIZATION OF MICROORGANISMS IN MICROBIAL COMMUNITIES
; FILE REFERENCE: 2139-33US
; CURRENT APPLICATION NUMBER: US/11/055,637
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,288
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe for DNA array
US-11-055-637-71

Query Match 53.6%; Score 817.2; DB 7; Length 1486;
Best Local Similarity 74.8%; Pred. No. 1.9e-254;
Matches 1105; Conservative 0; Mismatches 356; Indels 16; Gaps 6;

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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              ||||||  || ||| |||||||||||||||| |       |    ||||||||  || |
Db         11 GGCGGCGTGCCTAATACATGCAAGTCGAGCGAACTGATTAGAAGCTTGCTTCTATGACGT 70

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              ||| || |   ||      |   | | || || |||   ||   |||||| ||  ||
Db         71 TAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGCCTGTAAGACTGGGATAACTTCGG 130

Qy        150 GAAACTCGAATTAATACCGCATA----------CGTCTACGGGAGAAAGCAGGGGNTCAT 199
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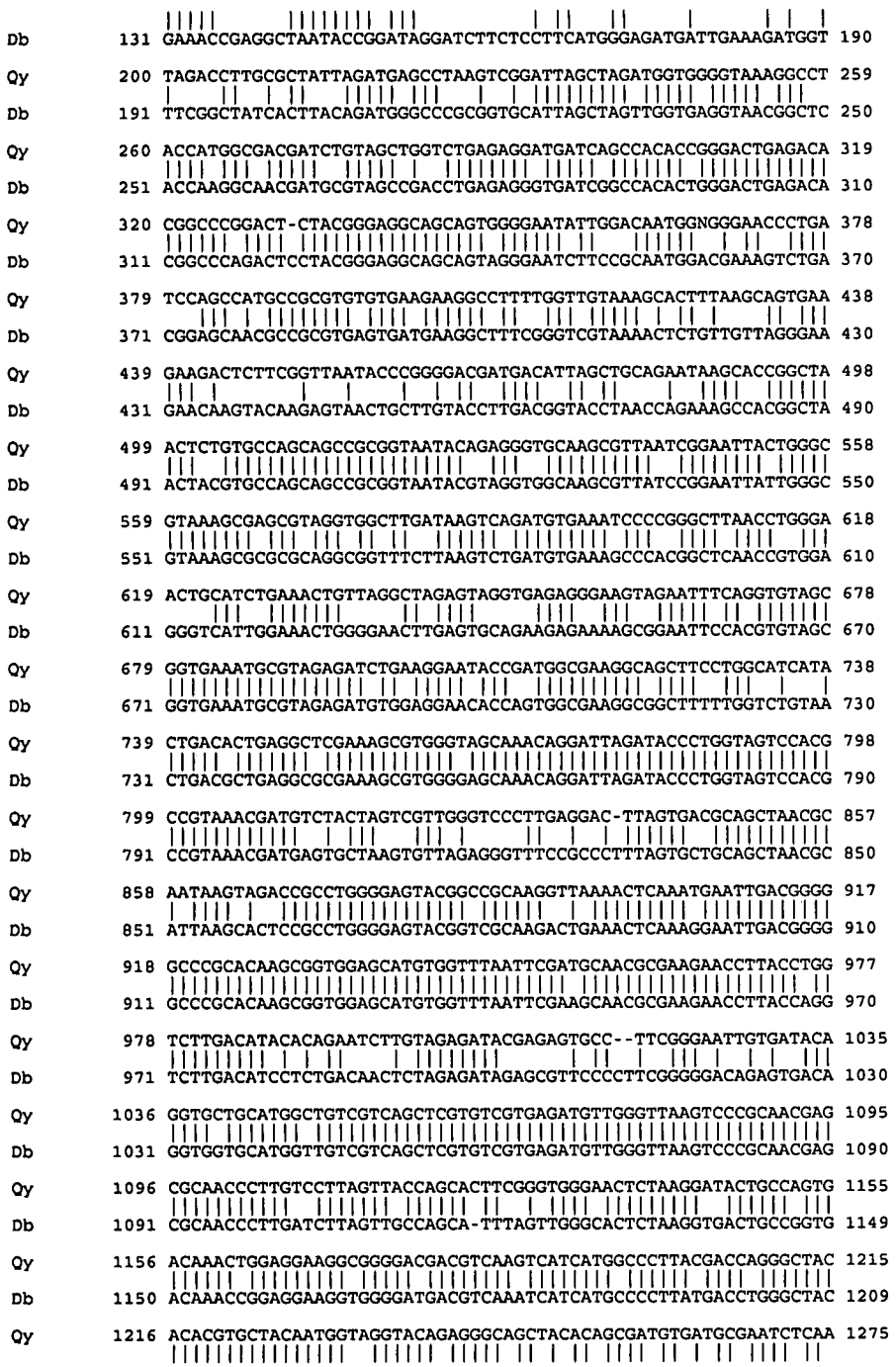

Search completed: December 3, 2005, 03:26:49
Job time : 258.827 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 2, 2005, 23:29:37 ; Search time 1618.84 Seconds
(without alignments)
7795.112 Million cell updates/sec

Title: US-09-979-558A-1
Perfect score: 1526
Sequence: 1 tttgatcatggctccagatt.....acctgcggctggatcacctc 1526

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	1211	79.4	269223	7	US-10-672-787-41	Sequence 41, Appl
	2	1098.6	72.0	1501	3	US-09-745-476-1	Sequence 1, Appli
	3	1098.6	72.0	1501	3	US-09-821-016-5	Sequence 5, Appli
	4	1098.6	72.0	1501	3	US-09-748-205-1	Sequence 1, Appli
	5	1098.6	72.0	1501	3	US-09-793-920A-1	Sequence 1, Appli
	6	1098.6	72.0	1501	3	US-09-951-720-1	Sequence 1, Appli
	7	1098.6	72.0	1501	3	US-09-791-610-1	Sequence 1, Appli
	8	1098.6	72.0	1501	5	US-10-218-519-5	Sequence 5, Appli
	9	1098.6	72.0	1501	5	US-10-266-787-5	Sequence 5, Appli
	10	1098.6	72.0	1501	5	US-10-252-518-5	Sequence 5, Appli
	11	1098.6	72.0	1501	5	US-10-105-305-1	Sequence 1, Appli
	12	1098.6	72.0	1501	5	US-10-133-404A-1	Sequence 1, Appli
	13	1098.6	72.0	1501	6	US-10-242-696-1	Sequence 1, Appli
	14	1098.6	72.0	1501	6	US-10-411-319-1	Sequence 1, Appli
	15	1098.6	72.0	1501	7	US-10-649-646-1	Sequence 1, Appli
	16	1098.6	72.0	1501	7	US-10-603-996-1	Sequence 1, Appli
	17	1098.6	72.0	1501	8	US-10-827-670-1	Sequence 1, Appli
	18	1090.4	71.5	1494	5	US-10-007-725-5	Sequence 5, Appli
	19	1073.8	70.4	1481	3	US-09-737-297-4	Sequence 4, Appli
	20	1070.8	70.2	1467	3	US-09-726-774-3	Sequence 3, Appli
	21	1070.8	70.2	1467	7	US-10-719-633-3	Sequence 3, Appli
	22	1070.6	70.2	1541	3	US-09-027-439-7	Sequence 7, Appli
	23	1070.2	70.1	1542	7	US-10-361-002-6	Sequence 6, Appli
	24	1070.2	70.1	1542	7	US-10-361-004-6	Sequence 6, Appli
	25	1070	70.1	1534	6	US-10-029-397A-35	Sequence 35, Appl
	26	1069.2	70.1	1542	3	US-09-940-925A-158	Sequence 158, App
	27	1069.2	70.1	1542	3	US-09-941-193A-158	Sequence 158, App
	28	1069.2	70.1	1542	5	US-10-061-071-33	Sequence 33, Appl
	29	1069.2	70.1	1542	9	US-10-723-365B-29	Sequence 29, Appl
	30	1069.2	70.1	1542	9	US-10-409-594-158	Sequence 158, App
	31	1069.2	70.1	1542	10	US-11-069-442-33	Sequence 33, Appl
c	32	1066.2	69.9	10903	7	US-10-612-224-1	Sequence 1, Appli
c	33	1065.2	69.8	11918	7	US-10-612-224-2	Sequence 2, Appli
	34	1065.2	69.8	13278	7	US-10-612-224-3	Sequence 3, Appli
	35	1062.6	69.6	1541	3	US-09-726-774-2	Sequence 2, Appli
	36	1062.6	69.6	1541	7	US-10-719-633-2	Sequence 2, Appli
	37	1062	69.6	1541	9	US-10-972-530-8	Sequence 8, Appli
	38	1058.2	69.3	1549	3	US-09-912-020-89	Sequence 89, Appl
	39	1058.2	69.3	1549	3	US-09-912-020-242	Sequence 242, App
	40	1058.2	69.3	1549	3	US-09-912-020-402	Sequence 402, App
	41	1058.2	69.3	1549	8	US-10-771-241-89	Sequence 89, Appl
	42	1058.2	69.3	1549	8	US-10-771-241-242	Sequence 242, App
	43	1058.2	69.3	1549	8	US-10-771-241-402	Sequence 402, App
	44	1052.4	69.0	1487	3	US-09-726-774-14	Sequence 14, Appl
	45	1052.4	69.0	1487	7	US-10-719-633-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-672-787-41/c
; Sequence 41, Application US/10672787
; Publication No. US20040067554A1
; GENERAL INFORMATION:
; APPLICANT: LAGACE, Robert, E.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BERG, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: ELITRA.025C1
; CURRENT APPLICATION NUMBER: US/10/672,787
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 09/596,002
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 41
; LENGTH: 269223
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-10-672-787-41

Query Match 79.4%; Score 1211; DB 7; Length 269223;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 127; Indels 15; Gaps 6;

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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
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Db      92956 GGCGGCAGGCTTAACACATGCAAGTCGAACG--AAGTTAGGAAGCTTGC--TTCTGATAC 92901

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
                | ||||||||||||||||| |||||||||| |||||||||||||||||| || |||
Db      92900 TTAGTGGCGGACGGGTGAGTAATGCTTAGGAATCTGCCTAGTAGTGGGGGATAACTTGGG 92841

Qy        150 GAAACTCGAATTAATACCGCATACGTCTACGGGAGAAAGCAGGGGNTCATTAGACCTTGC 209
              ||||| | |  ||||||||||||||| |    ||  ||  |||    || | || |
Db      92840 GAAACCCAAGCTAATACCGCATACGACCTACGGGTGAAAGGGGG----CTTTTAGCTCTC 92785

Qy        210 GCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCGA 269
              |||||||||||||||||||||||||||||| | ||||||||||||||||||| |||||
Db      92784 GCTATTAGATGAGCCTAAGTCGGATTAGCTGGTTGGTGGGGTAAAGGCCTACCAAGGCGA 92725

Qy        270 CGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGAC 329
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||| |||
Db      92724 CGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCCAGAC 92665
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Qy       330 T-CTACGGGAGGCAGCAGTGGGGAAT-----ATTGGACAATGGNGGGAACCCTGATCCAG 383
Db     92664 TCCTACGGGAGGCAGCAGTGGGGAATATTGGATTGGACAATGGGCGAAAGCCTGATCCAG 92605

Qy       384 CCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGA 443
Db     92604 CCATGCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGTGGGGAGGAAAA 92545

Qy       444 CTCTTCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCT 503
Db     92544 GCTTATGGTTAATACCCATAAGCCCTGACGTTACCCACAGAATAAGCACCGGCTAACTCT 92485

Qy       504 GTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAA 563
Db     92484 GTGCCAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAA 92425

Qy       564 GCGAGCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGC 623
Db     92424 GCGCGCGTAGGTGGTTATTTAAGTCAGATGTGAAAGCCCCGGGCTTAACCTGGGAACTGC 92365

Qy       624 ATCTGAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGA 683
Db     92364 ATCTGATACTGGATAACTAGAGTAGGTGAGAGGGGAGTAGAATTCCAGGTGTAGCGGTGA 92305

Qy       684 AATGCGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGAC 743
Db     92304 AATGCGTAGAGATCTGGAGGAATACCGATGGCGAAGGCAGCTCCCTGGCATCATACTGAC 92245

Qy       744 ACTGAGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA 803
Db     92244 ACTGAGGTGCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA 92185

Qy       804 AACGATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAG 863
Db     92184 AACGATGTCTACCAGTCGTTGGGTCTTTTAAAGACTTAGTGACGCAGTTAACGCAATAAG 92125

Qy       864 TAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGC 923
Db     92124 TAGACCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGC 92065

Qy       924 ACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGA 983
Db     92064 ACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGA 92005

Qy       984 CATACACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGC 1043
Db     92004 CATAGTGAGAATCTTGCAGAGATGCGAGAGTGCCTTCGGGAATTCACATACAGGTGCTGC 91945

Qy      1044 ATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC 1103
Db     91944 ATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC 91885

Qy      1104 TTGTCCTTAGTTACCAGCACTTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTG 1163
Db     91884 TTTTCCTTAGTTACCAGCGACTCGGTCGGGAACTCTAAGGATACTGCCAGTGACAAACTG 91825

Qy      1164 GAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGC 1223
Db     91824 GAGGAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGC 91765

Qy      1224 TACAATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTA 1283
Db     91764 TACAATGGTTGGTACAAAGGGTTGCTACACAGCGATGTGATGCTAATCTCAAAAAGCCAA 91705

Qy      1284 TCGTAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGC 1343
Db     91704 TCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAGTAATCGC 91645

Qy      1344 GGATCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT 1403
Db     91644 AGATCAGAATGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCAT 91585

Qy      1404 GGGAGTTGATTGCACCAGAAGTGGTTAGCCTAACTTAGTGAGGGCGATCACCACGGTGTG 1463
Db     91584 GGGAGTTGATCTCACCAGAAGTGGTTAGCCTAACGCA-AGAGGGCGATCACCACGGTGGG 91526

Qy      1464 GTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
Db     91525 GTCGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 91466

Qy      1524 CTC 1526
Db     91465 CTC 91463
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RESULT 2
US-09-745-476-1
; Sequence 1, Application US/09745476
; Patent No. US20010029039A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Preparation of Poly-hidroxyalkanoic Acid
; FILE REFERENCE: 4351008
; CURRENT APPLICATION NUMBER: US/09/745,476
; CURRENT FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-09-745-476-1

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.6e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Qy        30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db         9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy        90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db        67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy       150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
Db       124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy       209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
Db       184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy       269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
Db       244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy       329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
Db       304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy       388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
Db       364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy       448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
Db       424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy       508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
Db       484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy       568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
Db       544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603
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Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
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Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              ||||||  ||  |||||||  |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              |||||  |||||  |||||||  |||||||  ||||||||  ||||||||||||  ||||| ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||||  ||||||||||||||||||||  || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||  |  ||||||||||||  |||  ||||||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              ||||||||||||||||  |  ||||||  |||||||||  ||||||  |||||||||  ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              |||||  |||||  ||||||||||||||||||||||||||||||  ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              ||||||  ||||||||||  ||  |  ||||  |||  ||  ||||  ||  |||  ||  ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              ||||||  |||  |  ||||||||||||||||  |  ||||||  ||||||||||||||||||  |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              |||  |  ||||||||||||  |  |||  ||||  |||  |  ||||  ||  |  ||||||||||  |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
                |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 3
US-09-821-016-5
; Sequence 5, Application US/09821016
; Patent No. US20010046692A1
; GENERAL INFORMATION:
; APPLICANT: CANON INC.
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 4051021
; CURRENT APPLICATION NUMBER: US/09/821,016
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
; FEATURE:
US-09-821-016-5

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.6e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              ||||||||| |||||||||||||||||||||||  | ||  |  ||||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | |||||||||||||||| | |||||||| ||| |||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||        |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              ||||||  |||||||||||  |||||||||||||||  |||||  |||||  |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              ||||||  |||  |||||||||||||||||||||||  |||||  ||  ||||||||||||  ||  ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              ||  ||||||||||||||||||||||||||||||||||||||  |  ||  ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              ||||||||||||||||||  |||  | ||||||||||||||||  |  ||  ||||  |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |  ||||||  |  ||||  ||| |  ||||||||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||||| |||||||| ||||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||||  |  ||||||  || |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              ||||||  ||  |||||||  |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              |||||  |||||  |||||||  |||||||  |||||||||||||  |||||  ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
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Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 4
US-09-748-205-1
; Sequence 1, Application US/09748205
; Patent No. US20020022253A1
; GENERAL INFORMATION:
;  APPLICANT:  Canon Inc.
;  TITLE OF INVENTION:  Polyhydroxyalkanoate its manufacturing method, and microorganism
;  TITLE OF INVENTION:  those are used for the method.
;  FILE REFERENCE:  4351009
;  CURRENT APPLICATION NUMBER: US/09/748,205
;  CURRENT FILING DATE:  2000-12-27
;  NUMBER OF SEQ ID NOS:  1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain.
US-09-748-205-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263
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Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 5
US-09-793-920A-1
; Sequence 1, Application US/09793920A
; Patent No. US20020065389A1
; GENERAL INFORMATION:
; APPLICANT: Canon Inc.
; TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxythienylalkanoic acid as
; TITLE OF INVENTION: monomer unit, and method for producing the same.
; FILE REFERENCE: 4396021
; CURRENT APPLICATION NUMBER: US/09/793,920A
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain.
US-09-793-920A-1

Query Match 72.0%; Score 1098.6; DB 3; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.6e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;

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Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
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Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 6
US-09-951-720-1
; Sequence 1, Application US/09951720
; Patent No. US20020160467A1
; GENERAL INFORMATION:
; APPLICANT: Canon Kabushiki Kaisha

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;  TITLE OF INVENTION: Polyhydroxyalkanoate and Manufacturing Method Thereof
;  FILE REFERENCE: 4477001
;  CURRENT APPLICATION NUMBER: US/09/951,720
;  CURRENT FILING DATE:  2000-09-14
;  PRIOR APPLICATION NUMBER: JP 279900/2000
;    JP 378827/2000
;    JP 165238/2001
;    JP 165509/2001
;    JP 275063/2001
;  PRIOR FILING DATE: 2000-09-14
;    2000-12-13
;    2001-05-31
;    2001-05-31
;    2001-09-11
;  NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii P161 strain.
US-09-951-720-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||||  | || |  |||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | |||||||||||||||| | ||||||||| ||| |||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||||| ||||| ||||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||| ||||| || |||||||||| || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || |||||||||||||||||||||||||||||||||||  | || ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||  | |||||||||||||||  | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |     |||| ||| |  ||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||| |||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||| |  ||||||  || |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              |||||| ||  |||||| |||  |||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              ||||| |||||  |||||||  |||||||  ||||||| |||||||||||| ||||| ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||||| |||||||||||||||||| || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | |||||||||||||   ||| ||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              |||||||||||||||  |   |||||| |||||||||| |||||| |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| |||||  |||||||||||||||||||||||||| || ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              |||||| ||||||||||  || |  | |||| |||  || |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              |||||| ||| | |||||||||||||| | |||||| |||||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | |||||||||||||| | ||| |||| ||| | |||| || | |||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 7
US-09-791-610-1
; Sequence 1, Application US/09791610
; Publication No. US20030100084A1
; GENERAL INFORMATION:
;  APPLICANT: Canon Inc.
;  TITLE OF INVENTION: Polyhydroxyalkanoate containing 3-hydroxybenzoylalkanoic acid as
;  TITLE OF INVENTION:  monomer unit, and method for producing the same.
;  FILE REFERENCE: 4396021
;  CURRENT APPLICATION NUMBER: US/09/791,610
;  CURRENT FILING DATE:  2002-09-30
;  NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain.
US-09-791-610-1

  Query Match             72.0%;  Score 1098.6;  DB 3;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
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  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||||||  | || |  ||||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | ||||||||||||||| | |||||||| ||| ||||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||| ||||| ||||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||| ||||| || |||||||||| || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || |||||||||||||||||||||||||||||||||||  | || ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||  | |||||||||||||||||  | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |  ||||||    |      |||| ||| |  ||||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||| |||||||| ||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              |||||| | |||||||| |  ||||||  || |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              |||||| ||  |||||||| |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              ||||| ||||| |||||||  |||||||  ||||||| ||||||||||||| ||||| ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||| |||||||||||||||||| || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||   ||| ||||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              |||||||||||||||| |    |||||| |||||||||| |||||| |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              |||||| |||||||||||  || |  | |||| |||  || |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              |||||| ||| | |||||||||||||||| | |||||| ||||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | |||||||||||||| | ||| |||| ||| | |||| || | ||||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
                 |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501
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RESULT 8
US-10-218-519-5
; Sequence 5, Application US/10218519
; Publication No. US20030049806A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya
; APPLICANT: Imamura, Takeshi
; APPLICANT: Suda, Sakae
; APPLICANT: Honma, Tsutomu
; TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
; FILE REFERENCE: 03500.015225.1
; CURRENT APPLICATION NUMBER: US/10/218,519
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/821,016
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii P161 ; BP-7376
; FEATURE:
; FEATURE: cDNA to 16S rRNA
US-10-218-519-5

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  Query Match             72.0%;  Score 1098.6;  DB 5;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||||||  | || |  ||||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | ||||||||||||||| | |||||||| ||| ||||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||| ||||| ||||| |||  |||| ||||
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Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||||| ||||| || |||||||||||| || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || ||||||||||||||||||||||||||||||||||||   | || ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||  | ||||||||||||||||  | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |    |||| ||| |  ||||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||| |||||||| ||||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||| |  ||||||  || |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              |||||| ||  |||||||| |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              ||||| ||||| |||||||  |||||||  |||||||| |||||||||||| ||||| ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||| |||||||||||||||||| || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||   ||| ||||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              |||||||||||||||| |    |||||| |||||||| |||||| |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| ||||| ||||||||||||||||||||||| || ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              |||||| ||||||||||  || |  | |||| ||  || |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              |||||| ||| | |||||||||||||||| | |||||| |||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | |||||||||||||| | ||| |||| ||| | |||| || | ||||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 9
US-10-266-787-5
; Sequence 5, Application US/10266787
; Publication No. US20030082777A1
; GENERAL INFORMATION:
;  APPLICANT: Yano, Tetsuya
;  APPLICANT:  Imamura, Takeshi
;  APPLICANT:  Suda, Sakae
;  APPLICANT:  Honma, Tsutomu
;  TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
;  FILE REFERENCE: 03500.015225.3
;  CURRENT APPLICATION NUMBER: US/10/266,787
;  CURRENT FILING DATE:  2002-10-09
;  PRIOR APPLICATION NUMBER: JP 2000-095004
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Microsoft Word
; SEQ ID NO 5
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii P161 ; BP-7376
;   FEATURE:
;   FEATURE: cDNA to 16S rRNA
US-10-266-787-5

  Query Match            72.0%;  Score 1098.6;  DB 5;  Length 1501;
  Best Local Similarity  85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||  | || |  |||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | |||||||||||||||| | ||||||||| ||| ||||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||||| ||||| ||||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||||| ||||| || |||||||||||| || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || ||||||||||||||||||||||||||||||||||||   | || ||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||  | ||||||||||||||||  | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |    |||| ||| |  ||||||||||||||||||||||||||
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Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501

RESULT 10
US-10-252-518-5
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; Sequence 5, Application US/10252518
; Publication No. US20030087413A1
; GENERAL INFORMATION:
;  APPLICANT: Yano, Tetsuya
;  APPLICANT:  Imamura, Takeshi
;  APPLICANT:  Suda, Sakae
;  APPLICANT:  Honma, Tsutomu
;  TITLE OF INVENTION: Polyhydroxyalkanoate Synthase and Gene Encoding the Same Enzyme
;  FILE REFERENCE: 03500.015225.2
;  CURRENT APPLICATION NUMBER: US/10/252,518
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: JP 2000-095004
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: Microsoft Word
; SEQ ID NO 5
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii P161 ; BP-7376
;   FEATURE:
;   FEATURE: cDNA to 16S rRNA
US-10-252-518-5

  Query Match             72.0%;  Score 1098.6;  DB 5;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
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Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 11
US-10-105-305-1
; Sequence 1, Application US/10105305
; Publication No. US20030096182A1
; GENERAL INFORMATION:
;  APPLICANT: CANON KABUSHIKI KAISHA
;  TITLE OF INVENTION: POLYHYDROXYALKANOATE CONTAINING UNIT WITH THIENYL STRUCTURE IN TH
;  TITLE OF INVENTION:  CHAIN, PROCESS FOR ITS PRODUCTION, CHARGE CONTROL AGENT, TONER E
;  TITLE OF INVENTION:  TONER WHICH CONTAIN THIS POLYHYDROXYALKANOATE, AND IMAGE-FORMING
;  TITLE OF INVENTION:  IMAGE-FORMING APPARATUS WHICH MAKE USE OF THE TONER
;  FILE REFERENCE: CFO16309
;  CURRENT APPLICATION NUMBER: US/10/105,305
;  CURRENT FILING DATE:  2002-03-26
;  PRIOR APPLICATION NUMBER: JP 2001-090026, JP 2001-133551
;  PRIOR FILING DATE: 2001-3-27, 2001-4-27
;  NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain.
US-10-105-305-1

  Query Match             72.0%;  Score 1098.6;  DB 5;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
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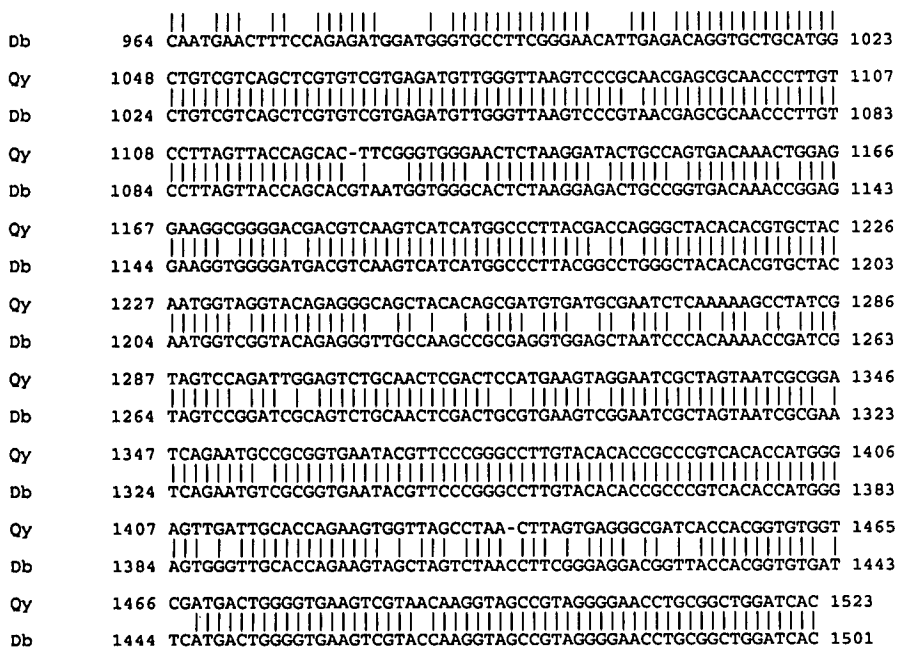
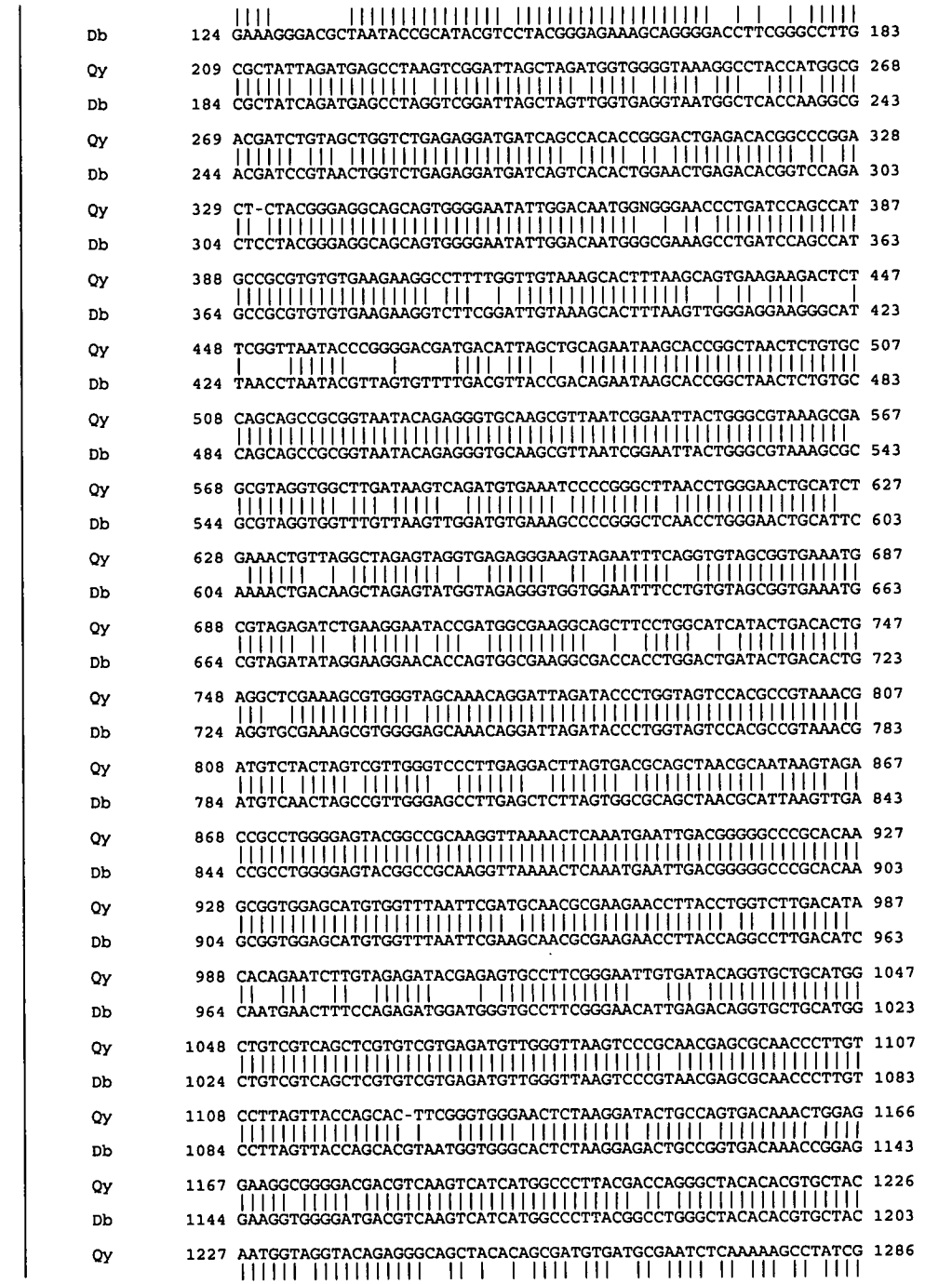


RESULT 12
US-10-133-404A-1
; Sequence 1, Application US/10133404A
; Publication No. US20030104302A1
; GENERAL INFORMATION:
; APPLICANT: Tsutomu Honma
; APPLICANT: Tetsuya Yano
; APPLICANT: Tsuyoshi No. US20030104302A1oto
; APPLICANT: Shinya Kozaki
; TITLE OF INVENTION: Construct and Method for Making It
; FILE REFERENCE: CFO16374
; CURRENT APPLICATION NUMBER: US/10/133,404A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: JP P2001-131694
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP P2001-208704
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Pseudomonas jessenii 161 strain
US-10-133-404A-1

Query Match 72.0%; Score 1098.6; DB 5; Length 1501;
Best Local Similarity 85.9%; Pred. No. 1.6e-288;
Matches 1287; Conservative 0; Mismatches 202; Indels 9; Gaps 6;



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Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              |||||| ||| | |||||||||||||||| | |||||| |||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | |||||||||||||| | ||| |||| ||| | |||| || | |||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
                |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 13
US-10-242-696-1
; Sequence 1, Application US/10242696
; Publication No. US20030180899A1
; GENERAL INFORMATION:
;  APPLICANT: Honma, Tsutomu
;  APPLICANT:  Kobayashi, Toyoko
;  APPLICANT:  Yano, Tetsuya
;  APPLICANT:  Kobayashi, Shin
;  APPLICANT:  Imamura, Takeshi
;  APPLICANT:  Suda, Sakae
;  APPLICANT:  Kenmoku, Takashi
;  TITLE OF INVENTION: Process for producing polyhydroxyalkanoate by utilizing microorga
;  FILE REFERENCE: 03500.015010.1
;  CURRENT APPLICATION NUMBER: US/10/242,696
;  CURRENT FILING DATE:  2002-09-13
;  PRIOR APPLICATION NUMBER: JP 11-371864
;  PRIOR FILING DATE: 12-27-1999
;  PRIOR APPLICATION NUMBER: JP 11-371867
;  PRIOR FILING DATE: 12-27-1999
;  PRIOR APPLICATION NUMBER: JP 11-371868
;  PRIOR FILING DATE: 12-27-1999
;  PRIOR APPLICATION NUMBER: JP 11-371869
;  PRIOR FILING DATE: 12-27-1999
;  PRIOR APPLICATION NUMBER: JP 2000-023024
;  PRIOR FILING DATE: 01-31-2000
;  PRIOR APPLICATION NUMBER: JP 2000-023025
;  PRIOR FILING DATE: 01-31-2000
;  PRIOR APPLICATION NUMBER: JP 2000-361323
;  PRIOR FILING DATE: 11-28-2000
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: Microsoft Word
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii P161 ; FERM P-17445
US-10-242-696-1

  Query Match             72.0%;  Score 1098.6;  DB 6;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy          30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
               |||||||||| |||||||||||||||||||  | || |  |||||||  |
Db           9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy          90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
               |    | |||||||||||||| | ||||||||| ||| |||||||||| | |
Db          67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy         150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
               ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db         124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy         209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
               |||||| |||||||||| |||||||||||||| ||||| ||||| ||| |||| ||||
Db         184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy         269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
               |||||| ||| |||||||||||||||||||| ||||| || |||||||||||| || ||
Db         244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy         329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
               || |||||||||||||||||||||||||||||||||  | || ||||||||||||||
Db         304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy         388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGCACTCT 447
               |||||||||||||||||||| ||| | |||||||||||||||| | || |||| |
Db         364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy         448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
               |    ||||||    |    |||| ||| |  ||||||||||||||||||||||||||
Db         424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy         508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy         568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
               |||||||||| ||| |||||  |||||||||| ||||||||||||||||||||||||
Db         544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy         628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
               ||||||  | |||||||| |  ||||||  || |||||||  ||||||||||||||||
Db         604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy         688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
               ||||||  ||  |||||| |||  |||||||||  |  |||||  | ||||||||||||
Db         664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy         748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
               |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy         808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
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Db         784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy         868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy         928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
               |||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db         904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy         988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
               ||  |||  ||  ||||||    | |||||||||||||   ||| ||||||||||||||
Db         964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy        1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
               |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy        1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
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Db        1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy        1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
               ||||| |||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy        1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
               |||||| |||||||||| || |  | |||| |||  || |||| || ||| || ||||
Db        1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy        1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
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Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 14
US-10-411-319-1
; Sequence 1, Application US/10411319
; Publication No. US20030208029A1
; GENERAL INFORMATION:
;  APPLICANT: Canon Inc.
;  TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms
;  TITLE OF INVENTION:  In The Same
;  FILE REFERENCE: 03500.015001.1
;  CURRENT APPLICATION NUMBER: US/10/411,319
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: US 09/748,205
;  PRIOR FILING DATE: 2000-12-27
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain
US-10-411-319-1

  Query Match             72.0%;  Score 1098.6;  DB 6;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89

Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149

Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208

Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268

Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328

Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387

Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447

Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507

Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567

Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627

Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687

Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747

Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807

Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867

Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927

Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987

Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047

Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107

Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166

Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226

Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286

Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346

Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406

Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465

Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523

Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501


RESULT 15
US-10-649-646-1
; Sequence 1, Application US/10649646
; Publication No. US20040067576A1
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; GENERAL INFORMATION:
;  APPLICANT: Canon Inc.
;  TITLE OF INVENTION: Polyhydroxynate, Method For Production Thereof And Microorganisms
;  TITLE OF INVENTION:  In The Same
;  FILE REFERENCE: 03500.015001.2
;  CURRENT APPLICATION NUMBER: US/10/649,646
;  CURRENT FILING DATE:  2003-08-28
;  PRIOR APPLICATION NUMBER: JP 11-371863
;  PRIOR FILING DATE: 1999-12-27
;  PRIOR APPLICATION NUMBER: JP 2000-023078
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: JP 2000-023080
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: JP 2000-023083
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: JP 2000-095011
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-095012
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-095013
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-207089
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: JP 2000-207091
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: JP 2000-359789
;  PRIOR FILING DATE: 2000-11-27
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1501
;   TYPE: DNA
;   ORGANISM: Pseudomonas jessenii 161 strain
US-10-649-646-1

  Query Match             72.0%;  Score 1098.6;  DB 7;  Length 1501;
  Best Local Similarity   85.9%;  Pred. No. 1.6e-288;
  Matches 1287;  Conservative    0;  Mismatches  202;  Indels    9;  Gaps    6;

Qy         30 GGCGGCAGGCTTAACACATGCAAGTCGAGCGGAAACGATGATAGCTTGCTATTAGGCGTC 89
              |||||||||| |||||||||||||||||||||  | || |  ||||||||  |
Db          9 GGCGGCAGGCCTAACACATGCAAGTCGAGCGG--ATGACGGGAGCTTGCTCCTGAATTCA 66

Qy         90 GAGCNGCCGGACGGGTGAGTAATACTTAGGAATCTACCTAGTAGTGGGGGATAGCTCGGG 149
              |    | |||||||||||||||| | ||||||||| ||| |||||||||| | |
Db         67 G---CGGCGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGACAACGTCTC 123

Qy        150 GAAACTCGAATTAATACCGCATACGT-CTACGGGAGAAAGCAGGGGNTCATTAGACCTTG 208
              ||||       |||||||||||||| ||||||||||||||||||  | |  | |||||
Db        124 GAAAGGGACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCTTG 183

Qy        209 CGCTATTAGATGAGCCTAAGTCGGATTAGCTAGATGGTGGGGTAAAGGCCTACCATGGCG 268
              |||||| |||||||||| |||||||||||||| ||||| |||| |||  |||| ||||
Db        184 CGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCG 243

Qy        269 ACGATCTGTAGCTGGTCTGAGAGGATGATCAGCCACACCGGGACTGAGACACGGCCCGGA 328
              |||||| ||| |||||||||||||||||||| ||||| || |||||||||||  || ||
Db        244 ACGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGA 303

Qy        329 CT-CTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGNGGGAACCCTGATCCAGCCAT 387
              || |||||||||||||||||||||||||||||||||  | || ||||||||||||||||
Db        304 CTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCAT 363

Qy        388 GCCGCGTGTGTGAAGAAGGCCTTTTGGTTGTAAAGCACTTTAAGCAGTGAAGAAGACTCT 447
              |||||||||||||||||| |||  | |||||||||||||||||  | || ||||    |
Db        364 GCCGCGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAT 423

Qy        448 TCGGTTAATACCCGGGGACGATGACATTAGCTGCAGAATAAGCACCGGCTAACTCTGTGC 507
              |    ||||||    |     |||| ||| |  |||||||||||||||||||||||||
Db        424 TAACCTAATACGTTAGTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGC 483

Qy        508 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGA 567
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CAGCAGCCGCGGTAATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGC 543

Qy        568 GCGTAGGTGGCTTGATAAGTCAGATGTGAAATCCCCGGGCTTAACCTGGGAACTGCATCT 627
              |||||||||| ||| |||||  |||||||| |||||||| ||||||||||||||||||
Db        544 GCGTAGGTGGTTTGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATTC 603

Qy        628 GAAACTGTTAGGCTAGAGTAGGTGAGAGGGAAGTAGAATTTCAGGTGTAGCGGTGAAATG 687
              ||||||  | |||||||||  |  ||||||  ||  |||||||  ||||||||||||||||
Db        604 AAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATG 663

Qy        688 CGTAGAGATCTGAAGGAATACCGATGGCGAAGGCAGCTTCCTGGCATCATACTGACACTG 747
              |||||| ||  |||||| |||  ||||||||||  |  |||||  | ||||||||||||
Db        664 CGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTG 723

Qy        748 AGGCTCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 807
              |||  |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        724 AGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACG 783

Qy        808 ATGTCTACTAGTCGTTGGGTCCCTTGAGGACTTAGTGACGCAGCTAACGCAATAAGTAGA 867
              ||||| |||||  |||||||  |||||||  |||||||  |||||||||||||  ||||| ||
Db        784 ATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGGCGCAGCTAACGCATTAAGTTGA 843

Qy        868 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 927
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 CCGCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAA 903

Qy        928 GCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATA 987
              |||||||||||||||||||||||||||||||||||||||||||||||||  || ||||||||
Db        904 GCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATC 963

Qy        988 CACAGAATCTTGTAGAGATACGAGAGTGCCTTCGGGAATTGTGATACAGGTGCTGCATGG 1047
              ||  |||  ||  ||||||    | ||||||||||||   ||| ||||||||||||||||
Db        964 CAATGAACTTTCCAGAGATGGATGGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGG 1023

Qy       1048 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGT 1107
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1024 CTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGTAACGAGCGCAACCCTTGT 1083

Qy       1108 CCTTAGTTACCAGCAC-TTCGGGTGGGAACTCTAAGGATACTGCCAGTGACAAACTGGAG 1166
              |||||||||||||||  |   |||||| |||||||||| |||||| |||||||| ||||
Db       1084 CCTTAGTTACCAGCACGTAATGGTGGGCACTCTAAGGAGACTGCCGGTGACAAACCGGAG 1143

Qy       1167 GAAGGCGGGGACGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTAC 1226
              ||||| |||||||||||||||||||||||||||||||| || ||||||||||||||||||
Db       1144 GAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGGCCTGGGCTACACACGTGCTAC 1203

Qy       1227 AATGGTAGGTACAGAGGGCAGCTACACAGCGATGTGATGCGAATCTCAAAAAGCCTATCG 1286
              |||||| ||||||||||  || |  | |||| |||  || |||| || ||| || ||||
Db       1204 AATGGTCGGTACAGAGGGTTGCCAAGCCGCGAGGTGGAGCTAATCCCACAAAACCGATCG 1263

Qy       1287 TAGTCCAGATTGGAGTCTGCAACTCGACTCCATGAAGTAGGAATCGCTAGTAATCGCGGA 1346
              |||||| ||| | |||||||||||||| | |||||| |||||||||||||||||||| |
Db       1264 TAGTCCGGATCGCAGTCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAGTAATCGCGAA 1323

Qy       1347 TCAGAATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1406
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 TCAGAATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGG 1383

Qy       1407 AGTTGATTGCACCAGAAGTGGTTAGCCTAA-CTTAGTGAGGGCGATCACCACGGTGTGGT 1465
              ||| | |||||||||||| | ||| |||| ||| | |||| || | ||||||||||| |
Db       1384 AGTGGGTTGCACCAGAAGTAGCTAGTCTAACCTTCGGGAGGACGGTTACCACGGTGTGAT 1443

Qy       1466 CGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1523
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       1444 TCATGACTGGGGTGAAGTCGTACCAAGGTAGCCGTAGGGGAACCTGCGGCTGGATCAC 1501

Search completed: December  3, 2005, 03:22:26
Job time : 1623.84 secs
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